

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 15:49:42 : Search time 4589 Seconds

(without alignments)
16913.747 Million cell updates/sec

Title: US-09-810-796-3

Perfect score: 2667

Sequence: 1 atgaagagatgtggagctcggg.....ctcatgtcaactgaatcaa 2667

Scoring table: IDENTITY_NUC
GapPen 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: gb_htg:*
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41: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a

Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
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| 1 | 2662.2 | 99.8 | 2772 | 6 | AX268474 Sequence |
| 2 | 2662.2 | 99.8 | 3111 | 6 | AX268476 Sequence |
| 3 | 2630 | 98.6 | 2694 | 6 | AX322509 Sequence |
| 4 | 2625.2 | 98.4 | 3137 | 6 | AX056817 Sequence |
| 5 | 2625.2 | 98.1 | 3137 | 6 | AF202977 Homo sapi |
| 6 | 2617.2 | 98.1 | 3074 | 6 | AX253254 Sequence |
| 7 | 2617.2 | 98.1 | 3074 | 6 | AX456864 Sequence |
| 8 | 2617.2 | 98.1 | 3074 | 6 | AF249278 Homo sapi |
| 9 | 2507.6 | 94.0 | 2832 | 9 | AF263835 Homo sapi |
| 10 | 2155 | 80.8 | 3108 | 10 | AF263836 Homo sapi |
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| 14 | 753.4 | 28.2 | 179192 | 2 | AC095904 Rattus no |
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| 17 | 492 | 18.4 | 2335 | 9 | AF105202 Sequence |
| 18 | 485.2 | 17.8 | 2827 | 10 | AB000497 Mus muscu |
| 19 | 475.2 | 17.8 | 2750 | 6 | AX456861 Sequence |
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| 21 | 473.2 | 17.7 | 2899 | 10 | AB000496 Homo sapi |
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| 23 | 465 | 17.4 | 548 | 6 | AX318576 Sequence |
| 24 | 465 | 17.4 | 548 | 6 | AX318764 Sequence |
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| 30 | 434 | 16.3 | 5927 | 10 | AF087454 Rattus no |
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| 39 | 423.4 | 15.9 | 1314 | 9 | BC000699 Homo sapi |
| 40 | 423.4 | 15.9 | 1425 | 6 | A94977 Sequence 4 |
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| 43 | 423 | 15.9 | 2014 | 10 | AB000501 Mus muscu |
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ALIGNMENTS

| RESULT 1 | AX268474 | 2772 bp | DNA | linear | PAT 29-OCT-2001 |
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| LOCUS | AX268474 | | | | |
| DEFINITION | Sequence 1 from Patent WO0175108. | | | | |
| ACCESSION | AX268474 | | | | |
| VERSION | AX268474.1 | GI:16541652 | | | |
| KEYWORDS | | | | | |
| SOURCE | human. | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| TITLE | Hu, Y., Kieck, J. A., Turner, A. C., Nehls, M. C., Friedrich, G. B., Zambrowicz, B. and Sands, A. T. Human ion channel protein and polynucleotides encoding the same | | | | |

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RESULT 2
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 LOCUS DEFINITION AX268476
 DEFINITION Sequence 3 from Patent WO0175108.
 VERSION AX268476.1 GI:16541653
 KEYWORDS human.
 SOURCE human.
 ORGANISM human sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 Hu, Y., Kieke, J.A., Turner, A.C., Nehls, M.C., Friedrich, G.B.,
 Zambrowicz, B. and Sands, A.T.
 Human Ion channel protein and polynucleotides encoding the same
 Patent: WO 0175108-A 3 11-OCT-2001;
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 /db_xref="taxon:9606"
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 Query Match 99.8%; Score 2662.2; DB 6; Length 3111;

Best Local Similarity 99.8%; Pred. No. 0;
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RESULT 4
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LOCUS Sequence 1 from Patent W0077035.
DEFINITION AX056817
ACCESSION AX056817.1 GI:12309758
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 3137)
Jentsch, T. J.
TITLE Novel potassium channels and genes encoding these potassium
channels
JOURNAL Patent: WO 0077035-A 1 21-DEC-2000;
NEUROSEARCH A/S (DK)
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BASE COUNT 865 a 749 c 745 g 778 t
ORIGIN

Query Match 98.4%; Score 2625.2; DB 6; Length 3137;
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LOCUS AF202977
DEFINITION Homo sapiens potassium voltage-gated channel, KQT-like subfamily,
member 5 (KCNO5) mRNA, complete cds.
ACCESSION AF202977
VERSION AF202977.1 GI:7798695
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE
1 (bases 1 to 3137)
Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
Jentsch,T.J.
KCNO5, a novel potassium channel broadly expressed in brain,
mediates M-type currents
J. Biol. Chem. 275 (31), 24089-24095 (2000)
PUBMED 10816588
JOURNAL
MEDLINE 20379054
AUTHORS
2 (bases 1 to 3137)
Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
Jentsch,T.J.
Direct Submission
Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistrasse
85, Hamburg 20246, Germany
FEATURES
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| Db | 2135 | TTATTCACATCAACTAGGCGCAACATCTCGAGAGGCGCTGCAGTTTCATTCTGAGCCCAAT | 2194 | | |
| QY | 1954 | GAGTTCAGTGGCCGACAGCTTCTTACGCGCTTACGCTTACTATGACAGTCAAGCAACAG | 2013 | | |
| Db | 2195 | GAGTTCAGTGGCCGACAGCTTCTTACGCGCTTACTATGACAGTCAAGCAACAG | 2254 | | |
| QY | 2014 | GTGCGCAATTAGTCAAAAGCGATGGCTGAGCAGTGGAGCCACCACACCGTTGCCAACCA | 2073 | | |
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| Db | 2375 | GCATTCAGAGATCTGGCCGACGAGCCGAGAAACTCTGACCTTAACCTGAGGCTTACAGGA | 2434 | | |
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| Db | 2435 | AGCATTTCTGACGTCCACCCTGCTTGGTCCCTCCAAAGGAAATTTTCAGATTGACAG | 2494 | | |
| QY | 2254 | TCAATCTCCACCAAGGACCGTTCTATGAGGAAAGCTTGAACATGGAGGAGAAACTCTG | 2313 | | |
| Db | 2495 | TCAATCTCCACCAAGGACCGTTCTATGAGGAAAGCTTGAACATGGAGGAGAAACTCTG | 2554 | | |
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| ACCESSION | AX456864.1 | GI:21715731 | | | |
| VERSION | | | | | |
| KEYWORDS | | | | | |
| SOURCE | Human. | | | | |
| ORGANISM | homo sapiens | | | | |
| | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| REFERENCE | 1 | Agentlieri, T.M. and Sheldon, J.H. | | | |
| AUTHORS | | Methods of selecting compounds for modulation of bladder function | | | |
| TITLE | | Patent: WO 0232960-A 5 25-Apr-2002; | | | |
| JOURNAL | | Wyeath (US) | | | |
| FEATURES | | Location/Qualifiers | | | |
| source | | I. .3074 | | | |

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| QY | 2254 | TCAATCTCACCAGAGACCGCTTCTATAGAGAAAAAGCTTTGACATGGAGAGAAACCTG | 2313 |
| Db | 2495 | TCAATCTCACCAGAGACCGCTTCTATAGAGAAAAAGCTTTGACATGGAGAGAAACCTG | 2554 |
| QY | 2314 | TTTCTGTCTGTCCATGGTGGCGAGAGACTTGGCAATCTTGTCTGTGCAAAACCTG | 2373 |
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| ACCESSION | AF249278 | | |
| VERSION | AF249278.1 | | |
| KEYWORDS | | | |
| SOURCE | Homo sapiens. | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. | | |
| REFERENCE | 1 (bases 1 to 3074) | | |
| AUTHORS | Lerche, C., Scherer, C.R., Seebom, G., Derst, C., Wei, A.D., Busch, A.E. and Steinmeyer, K. | | |
| TITLE | Molecular cloning and functional expression of KCNO5, a potassium channel subunit that may contribute to neuronal M-current diversity | | |
| JOURNAL | J. Biol. Chem. 275 (29), 22395-22400 (2000) | | |
| MEDLINE | 20357367 | | |
| PUBMED | 10787416 | | |
| REFERENCE | 2 (bases 1 to 3074) | | |
| AUTHORS | Lerche, C., Scherer, C.R., Seebom, G., Derst, C., Wei, A.D., Busch, A.E. and Steinmeyer, K. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (24-MAR-2000) Cardiovascular Diseases, Aventis Pharma Deutschland GmbH, Building H824, Frankfurt a. M. 65926, Germany | | |
| FEATURES | 1..3074 | | |
| SOURCE | /organism="Homo sapiens" | | |

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 Db 1861 CTGAGCGCCAAATGAGTTCAGTGGCCAGACTTTTACGCCCTTACTATGTCACAGT 1920
 QY 2002 CAGGCAACACAGGTGCCAATTAAGTCAAAAGGATGGCTCAGCAGTGGCAGCACACACACC 2061
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 Db 1921 CAGGCAACACAGGTGCCAATTAAGTCAAAAGGATGGCTCAGCAGTGGTAGGCCACCAACACC 1980
 QY 2062 ATTGCAANCAATTAATATGCGCAGCCCAAGCCAGCGACCCCAACACTTTACAGATCCCA 2121
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 Db 1981 ATTGCAANCAATTAATATGCGCAGCCCAAGCCAGCGACCCCAACACTTTACAGATCCCA 2040
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 Db 2041 CCTCTCTCCAGCCATCAAGCATCTGGCCAGGCCAGAAACCTGCAACCCCTGCA 2100
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 QY 2242 CAGGTTGACAGATCAATATCTCCCAAGGCGCTTCTATAGGAAAAAGCTTTGACATGGA 2301
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 QY 2302 GGAAGAACTCTGTTGCTGCTGTCCTCATGTTGCCAAGAGACTTGGGCAATCTTTGCTC 2361
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 Db 2221 GGAAGAACTCTGTTGCTGCTGTCCTCATGTTGCCAAGAGACTTGGGCAATCTTTGCTC 2280
 QY 2362 GTGCAAAAACCTGATCAGGTGACCGAGACACTGAATATATCAACTTTGAGGAGTGA 2421
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 Db 2281 GTGCAAAAACCTGATCAGGTGACCGAGACACTGAATATATCAACTTTGAGGAGTGA 2240
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Db 2401 ACTGATGAAGAGGTGGTCCCGAAGAGACAGACGACACTTTTGTATGCCGACCCGAG 2460
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 Db 2461 CTTGCCAGGAAAGCTGCTTGGATCAGACTCTCTAAGGACTGGAAAGTTCAGATCATCT 2520
 QY 2602 CAGAGCATTTGTAAAGGAGGAAAGTACAGATGCCCTGACCTTGCCTCATGTCAACTG 2661
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 Db 2521 CAGAGCATTTGTAAAGGAGGAAAGTACAGATGCCCTGACCTTGCCTCATGTCAACTG 2580
 QY 2662 AAATTA 2667
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 Db 2581 AAATTA 2586
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 AF263836 3108 bp mRNA linear ROD 01-JUN-2000
 LOCUS AF263836
 DEFINITION Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,
 partial cds.
 ACCESSION AF263836
 VERSION AF263836.1 GI:8132998
 KEYWORDS Mus musculus.
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3108)
 AUTHORS Kniazeva, M. and Han, M.
 TITLE A new gene of the voltage-gated potassium channel KCNQ family,
 KCNQ5, is a candidate gene for retinal disorders
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3108)
 AUTHORS Kniazeva, M. and Han, M.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
 Porter Biosciences Bldg., Boulder, CO 80309, USA
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 /strain="BALB/c"
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 GSRGSDPYKWRSEKLPFLTIDEVGAETETLDTDTGTPPPGAEAFSSDSLRTGSRSS
 SONICKTGDSTDLISLPHVKN"
 BASE COUNT 830 a 779 c 748 g 743 t 8 others

Query 2130 CCCAGCATCAAGCATCTGCCAGAGCCAGAACTCTGCACCCCTAACCCCTGCAGCTTACA 2189
Db 2101 CTCGGCCATCAAGCATCTGCCAGAGCCAGAACTCTGCCTCTCAAAACCCACCGCTTACA 2160
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Db 2161 AGAGGATTTTGTGATGTACACCTGCTTGTGCTTCCAAAGAAATTTGAGTTGC 2220
QY 2250 ACAGTCAATCTCACCAGAGAGCCGTTCTATGAGAAAGCTTTGACATGGAGAGAAC 2309
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QY 2310 TCTGTGTCTGTCTCTCCATGTGTGTCGAGAGACTTTGGCAATCTTTGTCTGTGAAAA 2369
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Db 2521 GGAAGTGGTGTCCGAGAGAGAGAGAGAGAGATTTTGTGTCGAGAGCCGCTGCGAG 2580
QY 2610 TTGTAAGGAGAGAGAGAGAGAGATTTTGTGTCGAGAGCCGCTGCGAG 2667
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RESULT 11
LOCUS HSA272519 1691 bp DNA linear PRI 21-FEB-2002
DEFINITION Homo sapiens partial KCON5 gene, exon 14.
ACCESSION AJ272519
VERSION AJ272519.1 GI:18873690
KEYWORDS KCON5 gene; KCON5 protein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Kanamura,C., Blevyerl,B., Hechenberger,M., Engels,H. and Steinlein,O.K.
TITLE The new voltage gated potassium channel KCON5 and early infantile convulsions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1691)
AUTHORS Steinlein,O.K.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Steinlein O.K., Institute of Human Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY
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286..1248
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/number=14
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BASE COUNT 508 a 397 c 337 g 448 t 1 others
ORIGIN

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Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1763 GGAAGAGTCCAGAGTCCAGAGTGGAGTGGCTTCTATGACATCTATCAACAGTCTTC 1822
Db 344 GGAAGAGTCCAGAGTCCAGAGTGGAGTGGCTTCTATGACATCTATCAACAGTCTTC 1822
QY 1823 AACGACATCTGACTATCAAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1882
Db 404 AACGACATCTGACTATCAAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1882
QY 1883 ACAGTGGCTGCTTATCCAGATCACTAGTCCAGATCTGAGAGAGTGGAGTGGAGTGGAG 1942
Db 464 ACAGTGGCTGCTTATCCAGATCACTAGTCCAGATCTGAGAGAGTGGAGTGGAGTGGAG 1942
QY 1943 TGAGGCAATGAGTTCAGTCCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2002
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QY 2123 CTCTCTCCAGAGTCCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2182
Db 704 CTCTCTCCAGAGTCCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2182
QY 2183 GCTTACAGAGATTTGAGTCCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2242
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Db 824 AGGTTCACAGTCAATTCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2302
QY 2303 GAGAACTCTGTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2362
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QY 2543 CTGAGGAGAGTGGTCCGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2602
Db 1124 CTGAGGAGAGTGGTCCGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2602
QY 2603 AGAGCATTTGTAAGCAG 2662
Db 1184 AGAGCATTTGTAAGCAG 2662
QY 2663 AATAA 2667
Db 1244 AATAA 1248

RESULT 12
AL365232
LOCUS
DEFINITION
Human DNA sequence from clone RP11-257K9 on chromosome 6, complete
sequence.
AL365232
ACCESSION
AL365232.24 GI:13234949
VERSION
HMG.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 120846)
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (01-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clonerequest@sanger.ac.uk
On Mar 5, 2001 this sequence version replaced gi:13160293.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Emi., EMBL; Sw.,
SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/MGP/Chr6
RP11-257K9 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-257K9. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP11-257K9 is at 1 in this sequence. The
true left end of clone RP1-319022 is at 120747 in this sequence.
The true right end of clone RP11-380M3 is at 18652 in this
sequence.

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8713..9200
/note="LTR repeat: matches 1. .568 of consensus"
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12067..12277

repeat_region
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18473..18730
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18829..19080
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19507..19632
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evidence=not_experimental
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25963..26384
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26891..27204
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32905..33039
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33040..33341
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37456. .37487
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Query Match 36.1%: Score 963.4; DB 9; Length 120846;
 Best local similarity 99.9%; Pred. No. 1.6e-236;
 Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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61339 AGGTACAGTCCATAGAGTCCAAAGCTGACCTGCTACTAGACTTATCAACAGGTCCTTC 61398
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1763 GGAAGAGCTCTGCTCAGCCCTGCTTTGGCTTCATTCAGATCCCACTTTTGATGTG 1822
|||||
61399 GGAAGAGCTCTGCTCAGCCCTGCTTTGGCTTCATTCAGATCCCACTTTTGATGTG 61458
|||||
1823 AACAGACATCTGACTATCAAGCCCTGCTGATAGCAAGATCTTGGGGTTCGCCAACA 1882
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61459 AACAGACATCTGACTATCAAGCCCTGCTGATAGCAAGATCTTGGGGTTCGCCAACA 61518
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QY 1883 ACAGTGGCTGCTTATCCAGATCAACATAGTGCACACATCTCGAGAGCCCTGACGTTTCATTC 1942
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Db 61519 ACAGTGGCTGCTTATCCAGATCAACATAGTGCACACATCTCGAGAGCCCTGACGTTTCATTC 61578
|||||
QY 1943 TGACGCCCAATGAGTTTCAGAGCCAGCTTTTACGGGCTTAGCCCTTACTATGACAGTC 2002
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Db 61579 TGACGCCCAATGAGTTTCAGAGCCAGCTTTTACGGGCTTAGCCCTTACTATGACAGTC 61638
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QY 2003 AAGCAGACAGAGTGGCCATTAATAGTCCAAAGAGATGCTTACAGAGTGGAGCCCAACACCA 2062
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Db 61639 AAGCAGACAGAGTGGCCATTAATAGTCCAAAGAGATGCTTACAGAGTGGAGCCCAACACCA 61698
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Db 61819 GCTTACAGAAAGCAATTTCTGACGTACACACACCTGTTGCTCCCAAGAAATGTTTC 61878
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RESULT 13
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 AC115920/c
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 AC115920
 VERSION AC115920.3 GI:21536151
 KEYWORDS
 HTG: HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 1 (bases 1 to 162123)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE
 Mus musculus, clone RP24-496HL

QY 1101 ----- 1100
Db 1220 GCCCTTGTGTTGAGCAGGTGCAAGGGCCCGCAATGGGGGCTACGGCCCTGGAGGTG 1279
QY 1101 ----- 1100
Db 1280 CGGGGGGGCGGTACCCGACGGAGACCCCTCCGTTACCCGGCCGTTGGCACCTGGCAC 1339
QY 1101 -----CTGACGCCCTTACCAATCAGAACTTAAGTTTAAAGAGCGA 1140
Db 1340 CGGGCGGGCAGCACCTCTCTTCTGCGCTGGGAAAGCAGCCGATGGGCATCAAGACCGC 1399
QY 1141 GTGGCGATGGCTAGGCCCAAGGGGCCAGAGTAT-----AAGACCAGCAAGCCTCAGTA 1194
Db 1400 ATCCGATGGGAGCTCCAGGGGGGGGCTCTTCAGAGCAGCTGGCACTTCA 1459
QY 1195 GGTGACAGAGGTCCCAAGCAGCCATCACAGCCAGG---GCACTCCCAACCAAGTG 1251
Db 1460 ACATGCCCCCTCCCAAGCAGCAGAGGTGGTGGGCCACAGCCACCAAGGTG 1519
QY 1252 CAGAAGAGCTGGAGCTTCAACGACGACCCGCTCGGCCCTGCTGCGCCTCAAAAGT 1311
Db 1520 CAAAAGAGCTGGAGCTCAATGACCGACCCGCTCGGGCATCTGAGACTC----- 1573
QY 1312 TCTCAGCCAAAACAGTGTAGATGCTGACACAGCCCTTGGCACTGATGATATATGAT 1371
Db 1574 -----AAACCCCGCCTCTGCTGAGGATGCC--CTTAGAGAGTAGCAGAG 1621
QY 1372 GAAAAGAGTGCAGTGTGATGTATCATGAGAGACCTCACCCACACCTTAAACTGTC 1431
Db 1622 GAGAAGAGCTACCACTGTAGCTCAGGTGGAGACATCATGCTGCTGTGAAGACAGTC 1681
QY 1432 ATTGAGCTATCAGAAATTGAAATTTCATGTTGCAAAACGAAAGTTAAAGAAACGTTA 1491
Db 1682 ATCCGCTCATCAGATGATCTCAAGTTCCTGTGGCCAAAGAAATTCAGAGACACTG 1741
QY 1492 CGTCCATATGATGTAAAGATGATGAACATATTCGTGTGATCTGACATGTTG 1551
Db 1742 CGACCTGACGAGGTGAAGACGTGATGACAGTACTCAGCAGGCCACCTGACATGCTG 1801
QY 1552 TGTAGAAATTAAAGCCTTCAACACGCTGTGATCAAAATCTTGGAAAAGGC---AAATC 1608
Db 1802 GGCGGATCAAGAGCCTGCAAACTCGGGTGGACCAATTTGGGTGGGGCCCGGGGAC 1861
QY 1609 ACATCAGATTAAGAGCCCGAGAGAAATPACGACAGACATGAGCCACAGACATCTC 1668
Db 1862 AGGAAGGCCCGGAGAAAGGCGCAAGGGGCCCTCCGACGCGAGGTGTGATGAATC 1921
QY 1669 AGTATGCTCGGTGGGTGTCAAGTTGAAAAACAGTACAGTCAATAGATCCAGCTG 1728
Db 1922 AGCATGATGGGAGCGGTGTCAAGGTGGAGAACAGGTGCAATGATCGACACAGCTG 1981
QY 1729 GACTGCCCTACTAGACATCTATCAACAGGTCTTGGAAAGGCTCTGCTCAGCCCTGCT 1788
Db 1982 GACCTGTGTTGGGTCTTATTCGCGCTGCTG-----GCTGTGGACCTTCGGCCAGC 2035
QY 1789 TTGCTTATTCAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCT 1848
Db 2036 CTGGGCGCGCTGCAAGTGGCGGCTGTGACCCGACATCACTCCGACTACACAGCCCT 2095
QY 1849 GTGATAGAAAGATCTTTCGGGTTCCGACAAA 1882
Db 2096 GTGGACACGAGGACATCTCCGTCTCCGACAGA 2129

Search completed: January 11, 2003, 17:21:14
Job time : 4901 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 15:46:12 : Search time 367 Seconds
(without alignments)
16365.339 Million cell updates/sec

Title: US-09-810-796-3

Perfect score: 2667
Sequence: 1 atgaagatgttgatcgcg.....ctcatgtcaactgaactaata 2667

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|----------|---------------------|
| 1 | 2667 | 100.0 | 2667 | 22 | AA514653 | Human CDNA encoding |
| 2 | 2662.2 | 99.8 | 2772 | 22 | AAH43633 | Human ion-channel |
| 3 | 2662.2 | 99.8 | 3111 | 22 | AAH43634 | Human ion-channel |
| 4 | 2630 | 98.6 | 2694 | 22 | AA514652 | Human CDNA encoding |
| 5 | 2630 | 98.6 | 2694 | 24 | AAD27192 | Human potassium ch |
| 6 | 2626.4 | 98.5 | 3071 | 22 | AA514651 | Human CDNA for vol |
| 7 | 2625.2 | 98.4 | 3137 | 22 | AAC85414 | Human KCNQ5 potass |
| 8 | 2617.2 | 98.1 | 3074 | 22 | AAH49499 | Human KCNQ5 DNA. |
| 9 | 2521 | 94.5 | 3718 | 21 | AA634371 | Human KCNQ5 (KCNQ5 |

| | | | | | | |
|----|-------|------|--------|----|----------|--------------------|
| 10 | 963.4 | 36.1 | 125910 | 21 | AA654370 | Human KCNQ5 (KCNQ5 |
| 11 | 492 | 18.4 | 2335 | 21 | AAH47618 | KCNQ4 potassium ch |
| 12 | 489.2 | 18.3 | 2273 | 20 | AAH57140 | Mouse KCNQ2 cDNA. |
| 13 | 475.6 | 17.8 | 2169 | 20 | AAH26588 | Nucleotide sequenc |
| 14 | 465 | 17.4 | 548 | 24 | ABA90234 | Human ORF41 coding |
| 15 | 452.2 | 17.0 | 7413 | 23 | AA574832 | DNA encoding novel |
| 16 | 447 | 16.8 | 2565 | 20 | AAH81548 | Human brain-derive |
| 17 | 447 | 16.4 | 3195 | 23 | AA574831 | DNA encoding novel |
| 18 | 436.6 | 16.4 | 3029 | 20 | AAH81547 | Human brain-derive |
| 19 | 427.2 | 16.0 | 2565 | 20 | AAH26596 | Nucleotide sequenc |
| 20 | 427.2 | 16.0 | 2914 | 20 | AAH57059 | Human KCNQ3 cDNA. |
| 21 | 426.8 | 16.0 | 2814 | 20 | AAH57141 | Mouse KCNQ3 cDNA. |
| 22 | 425 | 15.9 | 3287 | 20 | AAH26587 | Nucleotide sequenc |
| 23 | 423.4 | 15.9 | 1182 | 18 | AAH85964 | Human K+ channel g |
| 24 | 423.4 | 15.9 | 1425 | 20 | AAH64418 | Human benign pros |
| 25 | 423.4 | 15.9 | 3232 | 20 | AAH57057 | Human KCNQ2 cDNA. |
| 26 | 423.4 | 15.9 | 3237 | 20 | AAH57145 | Human mutant KCNQ2 |
| 27 | 423 | 15.9 | 3232 | 23 | AA574830 | DNA encoding novel |
| 28 | 409.2 | 15.3 | 414 | 24 | AAH24166 | Human ORF1 polynuc |
| 29 | 361 | 13.5 | 2900 | 22 | AAH99526 | Human protein enco |
| 30 | 361 | 13.5 | 2911 | 23 | AA573267 | DNA encoding novel |
| 31 | 361 | 13.5 | 4154 | 23 | AAH83921 | DNA encoding novel |
| 32 | 331 | 12.4 | 735 | 20 | AAH26589 | Nucleotide sequenc |
| 33 | 312.4 | 11.7 | 1320 | 23 | AA573266 | DNA encoding novel |
| 34 | 312.4 | 11.7 | 1320 | 23 | AAH83917 | DNA encoding novel |
| 35 | 307.6 | 11.5 | 1566 | 23 | AA567245 | DNA encoding novel |
| 36 | 307.6 | 11.5 | 1566 | 23 | AAH84027 | DNA encoding novel |
| 37 | 285.4 | 10.7 | 1280 | 23 | ABL28585 | DNA encoding novel |
| 38 | 267.8 | 10.0 | 2028 | 22 | AAH30824 | Human KVLQT1 gene. |
| 39 | 267.8 | 10.0 | 3181 | 21 | AAZ90669 | Human KVLQT1 prote |
| 40 | 267.8 | 10.0 | 3181 | 21 | AAZ98901 | Human long QT synd |
| 41 | 267.8 | 10.0 | 3181 | 22 | AAH89911 | Human KVLQT1 codin |
| 42 | 266.6 | 10.0 | 2734 | 22 | AAH89984 | Mutant human KVLQT |
| 43 | 266.6 | 10.0 | 2821 | 18 | AAH94004 | DNA encoding human |
| 44 | 266.6 | 10.0 | 2821 | 18 | AAH90730 | Human KVLQT1 full- |
| 45 | 266.6 | 10.0 | 2821 | 24 | ABN96861 | Gene #3359 used to |

ALIGNMENTS

RESULT 1
ID AAS14653 standard; cDNA; 2667 BP.
XX AAS14653:
XX
XX 18-DEC-2001 (first entry)
XX
XX
XX Human CDNA encoding a voltage gated potassium channel hKVN5-2.
DE Human: ss. voltage-gated potassium channel; KCNQ5-2; nontropic;
KW cerebrotectic; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder;
KW stroke; pain; gene therapy; splice variant.
XX
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
FH 1..2967
FT CDS /tag= a
FT /product= "hKCNQ5-2"
XX
XX
XX MO200170759-A1.
XX
XX 27-SEP-2001.
XX
XX 20-MAR-2001; 2001WO-US09328.
XX
XX 21-MAR-2000; 2000US-190954P.
XX
XX (ICAG-) ICAGEN INC.

XX Jiegla TJ:
 XX WPI: 2001-611467/70.
 DR P-PSDB: AAU09021.
 XX
 PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ alpha
 PT subunits
 XX
 XX
 PS Claim 5: Page 63-64; 78pp; English.
 CC The invention relates to an isolated polypeptide comprising an
 CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
 CC 638 sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a splice variant of hKCNQ5 encoding hKCNQ5-2.
 XX
 XX
 SQ Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 other;
 Query Match 100.0%; Score 2667; DB 22; Length 2667;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 421 ATCATTCGAATCTGCTCTGCGGGTCTGCTGTTCGATATAGAGATGSCAAGAACTG 480
 QY 481 AGSTTTCGCGAAGAGCCCTTCTGTATAGATACCAATGTCTTATGCGTTCAATAGA 540
 DB 481 AGSTTTCGCGAAGAGCCCTTCTGTATAGATACCAATGTCTTATGCGTTCAATAGA 540
 QY 541 GTTGTTCGCAAAACCTCAGGGAATATATTTTCCACGTCTGCACCTCAGAGCTCCGT 600
 DB 541 GTTGTTCGCAAAACCTCAGGGAATATATTTTCCACGTCTGCACCTCAGAGCTCCGT 600
 QY 601 TTCCTACAGATCTCTCCGATGCTGCGCATGAGACCGAAGGGAGCAGCTTGAATACG 660
 DB 601 TTCCTACAGATCTCTCCGATGCTGCGCATGAGACCGAAGGGAGCAGCTTGAATACG 660
 QY 661 GGTTCAGTGGTTATGTCACAGCAGAGAAATTAATCACAGCTGGTATAGATTTTGG 720
 DB 661 GGTTCAGTGGTTATGTCACAGCAGAGAAATTAATCACAGCTGGTATAGATTTTGG 720
 QY 721 GTTCTATTTTTCGTCCTTCTGTCATCTGTGTAAGAAAGATGCCAATTAAGAGTTT 780
 DB 721 GTTCTATTTTTCGTCCTTCTGTCATCTGTGTAAGAAAGATGCCAATTAAGAGTTT 780
 QY 781 TCTACATATCAGATGCTCTCTGTGGGCGCAATTAATGACACTATTTGGCTATGGA 840
 DB 781 TCTACATATCAGATGCTCTCTGTGGGCGCAATTAATGACACTATTTGGCTATGGA 840
 QY 841 GACAAACCTCCCTAATCTTGGCTGGAAGATTGCTTCTGACAGGCTTTCACCTCTGGC 900
 DB 841 GACAAACCTCCCTAATCTTGGCTGGAAGATTGCTTCTGACAGGCTTTCACCTCTGGC 900
 QY 901 ATTTCTTTCTTTGACATCTCTGCGGCAATCTTGAGCTGAGTTTGCATTAAGATCAA 960
 DB 901 ATTTCTTTCTTTGACATCTCTGCGGCAATCTTGAGCTGAGTTTGCATTAAGATCAA 960
 QY 961 GAACACACCGCCGAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCAACCTCATTCAG 1020
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 DB 1141 GTGCGCATGGCTAGCCCGAAGGGCGCAGAGTAAAGACCCGACAGCCGACATAGGTGAC 1200
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 DB 1201 AGGAGTCCCCAAGCAGACATACAGCCGAGGCGAGTCCACCAAAAGTGCAGAGAC 1260
 QY 1261 TGGAGCTTCAACGACGACACCCGCTTCGCGCCTGCTGCGCTTAAAGTTCTAGGCA 1320
 DB 1261 TGGAGCTTCAACGACGACACCCGCTTCGCGCCTGCTGCGCTTAAAGTTCTAGGCA 1320
 QY 1321 AAACCACTGATGATGTCGACACAGCCCTTGGCACTGATGATGATGATGATGATGATG 1380
 DB 1321 AAACCACTGATGATGTCGACACAGCCCTTGGCACTGATGATGATGATGATGATGATG 1380
 QY 1381 TGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 DB 1381 TGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
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 QY 1501 GATGTAAGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
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Dh 166 GACGCGCTGCTACTGCTGGGACACCCGCGCGCCACGCTCGTGGCGGCGGTGGGCTG 225
Oy 121 AGGAGAGCGCGCGGGGGAAGAGGGGGCGCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Dh 226 AGGAGAGCGCGCGGGGGAAGAGGGGGCGCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 285
Oy 181 TACACGAGTAGCCAGAGAGCTGGCGGCGCAACGTCAAGTACCGGGGGTGCAGAACTACTG 240
Dh 286 TACACGAGTAGCCAGAGAGCTGGCGGCGCAACGTCAAGTACCGGGGGTGCAGAACTACTG 345
Oy 241 TACACGAGTAGCCAGAGAGCGCGGCGCTGGGCGTTCATCTACCAGCTTTCGTTTTCTC 300
Dh 346 TACACGAGTAGCCAGAGAGCGCGGCGCTGGGCGTTCATCTACCAGCTTTCGTTTTCTC 405
Oy 301 CTGTCTTGGTGGTGTGATTTGTCAGTGTTCAGCATCCCTAGCAGCAACAAATG 360
Dh 406 CTGTCTTGGTGGTGTGATTTGTCAGTGTTCAGCATCCCTAGCAGCAACAAATG 465
Oy 361 GCGCTAAGTTGCCCTCTTGATCTCGAGTTCTGTGATGATTCGTCCTTTGGTGGAGTTC 420
Dh 466 GCGCTAAGTTGCCCTCTTGATCTCGAGTTCTGTGATGATTCGTCCTTTGGTGGAGTTC 525
Oy 421 ATCATTCGAATCTGCTGCTCGGGGTTGCTGTTCATATAGAGATGGCAGAGAACTG 480
Dh 526 ATCATTCGAATCTGCTGCTCGGGGTTGCTGTTCATATAGAGATGGCAGAGAACTG 585
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Dh 946 GACAACATCCCTTAACCTTGGCTGGGAAGATGCTTTCAGAGCTTTCAGCTTGGC 1005
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Dh 1006 ATTTCTTCTTTCGACTTCGTCGCGCATTTCTGGCTCAGGTTTTCATTAAGTACAA 1065
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Oy 1201 AGAGGTCCCAAGCACCGCATTCAGCGGAGGCGAGTCCACCAAGTGCCAGAGAGC 1260
Dh 1306 AGGAGTCCCAAGCACCGCATTCAGCGGAGGCGAGTCCACCAAGTGCCAGAGAGC 1365
Oy 1261 TGGAGCTTCAACGAGCAACCCGCTTCGGGCTTCGGTGGCGCTCAAAAGTTCTCAGCA 1320
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Oy 1321 AANCCAGTATAGTCTGACACAGCCCTTGGCAGCTATGATGTATGATGAAGAAAAGA 1380
Dh 1426 AANCCAGTATAGTCTGACACAGCCCTTGGCAGCTATGATGTATGATGAAGAAAAGA 1485
Oy 1381 TGGCAGTGTGATGTATCAGTGAAGACCTCACCACCACTTAAGCTGATTCAGACT 1440
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Oy 1621 AAGAGCCGAGAGAAATTAACAGCAGAAATGAGACCAAGAGATCTCATGATGCTGGT 1680
Dh 1726 AAGAGCCGAGAGAAATTAACAGCAGAAATGAGACCAAGAGATCTCATGATGCTGGT 1785
Oy 1681 GGGGTGTAAAGGTTAAAAACAGTACAGTCCATAGTCCAAAGCTGAGATGCTTACTA 1740
Dh 1786 GGGGTGTAAAGGTTAAAAACAGTACAGTCCATAGTCCAAAGCTGAGATGCTTACTA 1845
Oy 1741 GACATCTATCAACAGGTCCTTCGAAAAGGCTTCGCTCAGCCCTCGCTTGGCTTCATTC 1800
Dh 1846 GACATCTATCAACAGGTCCTTCGAAAAGGCTTCGCTCAGCCCTCGCTTGGCTTCATTC 1905
Oy 1801 CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAA 1860
Dh 1906 CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAA 1965
Oy 1861 GATCTTGGGGTTCGCGACAAAACAGTGGCTGTATCCAGATCAACGTAGGCCAATC 1920
Dh 1966 GATCTTGGGGTTCGCGACAAAACAGTGGCTGTATCCAGATCAACGTAGGCCAATC 2025
Oy 1921 TCGAGAGGCTCGAGTTCAATTCGAGCGCAAAATGAGTTCAAGTGGCCAGACTTTCAGCG 1980
Dh 2026 TCGAGAGGCTCGAGTTCAATTCGAGCGCAAAATGAGTTCAAGTGGCCAGACTTTCAGCG 2085
Oy 1981 CTTAAGCCTTACTATGCAAGTCAAGCAACACAGGTGCCAATTACTCAAAAGCGATGCTCA 2040
Dh 2086 CTTAAGCCTTACTATGCAAGTCAAGCAACACAGGTGCCAATTACTCAAAAGCGATGCTCA 2145
Oy 2041 GGAGTGGCAGCCACCAACCAATTTGCAAAACCAATAATTAATACGCCCAACCGCAGCAGCC 2100
Dh 2146 GGAGTGGCAGCCACCAACCAATTTGCAAAACCAATAATTAATACGCCCAACCGCAGCAGCC 2205
Oy 2101 CCAACAACTTACAGATTCACACCTCCTTCGAGCCATCAAGCAATCTGACGAGCCAGAA 2160
Dh 2206 CCAACAACTTACAGATTCACACCTCCTTCGAGCCATCAAGCAATCTGACGAGCCAGAA 2265
Oy 2161 ACTGTGACCCCTAACCCTCGAGGCTTAACAGAAAAGCAATTTCTGACGTACACCTGCGCT 2220
Dh 2266 ACTGTGACCCCTAACCCTCGAGGCTTAACAGAAAAGCAATTTCTGACGTACACCTGCGCT 2325
Oy 2221 GTTGGCTCCAAGGAAATGTTCAGGTTTGCACAGTCAATCTCACCAAGGACCGTTCTATG 2280
Dh 2326 GTTGGCTCCAAGGAAATGTTCAGGTTTGCACAGTCAATCTCACCAAGGACCGTTCTATG 2385

| Accession | Gene | Species | Length (bp) | Source | Notes |
|-----------|--------|--------------|-------------|---------|------------|
| U01234 | hKv2.1 | Homo sapiens | 1920 | GenBank | Brain cDNA |
| U01235 | hKv2.1 | Homo sapiens | 1980 | GenBank | Brain cDNA |
| U01236 | hKv2.1 | Homo sapiens | 2144 | GenBank | Brain cDNA |
| U01237 | hKv2.1 | Homo sapiens | 2040 | GenBank | Brain cDNA |
| U01238 | hKv2.1 | Homo sapiens | 2204 | GenBank | Brain cDNA |
| U01239 | hKv2.1 | Homo sapiens | 2100 | GenBank | Brain cDNA |
| U01240 | hKv2.1 | Homo sapiens | 2264 | GenBank | Brain cDNA |
| U01241 | hKv2.1 | Homo sapiens | 2160 | GenBank | Brain cDNA |
| U01242 | hKv2.1 | Homo sapiens | 2324 | GenBank | Brain cDNA |
| U01243 | hKv2.1 | Homo sapiens | 2280 | GenBank | Brain cDNA |
| U01244 | hKv2.1 | Homo sapiens | 2444 | GenBank | Brain cDNA |
| U01245 | hKv2.1 | Homo sapiens | 2340 | GenBank | Brain cDNA |
| U01246 | hKv2.1 | Homo sapiens | 2504 | GenBank | Brain cDNA |
| U01247 | hKv2.1 | Homo sapiens | 2400 | GenBank | Brain cDNA |
| U01248 | hKv2.1 | Homo sapiens | 2564 | GenBank | Brain cDNA |
| U01249 | hKv2.1 | Homo sapiens | 2460 | GenBank | Brain cDNA |
| U01250 | hKv2.1 | Homo sapiens | 2624 | GenBank | Brain cDNA |
| U01251 | hKv2.1 | Homo sapiens | 2520 | GenBank | Brain cDNA |
| U01252 | hKv2.1 | Homo sapiens | 2684 | GenBank | Brain cDNA |
| U01253 | hKv2.1 | Homo sapiens | 2580 | GenBank | Brain cDNA |
| U01254 | hKv2.1 | Homo sapiens | 2744 | GenBank | Brain cDNA |
| U01255 | hKv2.1 | Homo sapiens | 2640 | GenBank | Brain cDNA |
| U01256 | hKv2.1 | Homo sapiens | 2804 | GenBank | Brain cDNA |
| U01257 | hKv2.1 | Homo sapiens | 267 | GenBank | Brain cDNA |
| U01258 | hKv2.1 | Homo sapiens | 2831 | GenBank | Brain cDNA |
| U01259 | hKv2.1 | Homo sapiens | 2831 | GenBank | Brain cDNA |
| U01260 | hKv2.1 | Homo sapiens | 2831 | GenBank | Brain cDNA |

as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5 polypeptides are useful for identifying compounds that modulate their biological activity. The compounds identified and KCNQ5 polynucleotides are useful for treating acute and chronic pain, migraine, acute stroke, dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders, depression, bipolar disorders, sleep disorders, eating disorders, addiction, myokymia, Alzheimer's disease, age-associated memory loss, learning deficiencies, cognitive disorders and motor neuron diseases. The nucleic acid molecules of the invention are further useful for treating neurophysiological, neuropsychological disorders, asthma, neuron cell death and brain tumours. They are also used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical excitability in the brain and are useful for generating antibodies. They are also useful to affinity purify biological effectors from biological materials e.g. disease tissues or cells. The present sequence is human KCNQ5 cDNA.

Sequence 2694 BP: 714 A: 671 C: 669 G: 640 T: 0 other:

Query Match 98.6%; Score 2630; DB 24; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

1 ATGAAGATGTGGAGTGGCGGGCGGGGCGAGGTGCTCTGTAACCTGGCAGCGCGAGGGG 60
1 ATGAAGATGTGGAGTGGCGGGCGGGGCGAGGTGCTCTGTAACCTGGCAGCGCGAGGGG 60
61 GACGGCTGTACTGCTGCTGGGACCCGCGCGGCGACGCTTGTTGGCGCGCGGTGGGCTG 120
61 GACGGCTGTACTGCTGCTGGGACCCGCGCGGCGACGCTTGTTGGCGCGCGGTGGGCTG 120
121 AGGAGAGACCCCGGGGCGAGAGGGGGCCGCGATGAGCCTCTGCGGGAAGCCGCTCTCT 180
121 AGGAGAGACCCCGGGGCGAGAGGGGGCCGCGATGAGCCTCTGCGGGAAGCCGCTCTCT 180
181 TACACGATGATCCAGAGAGTGGCGGGCGCAACGTAAGTACCGCGGGTGGAGACTACCTG 240
181 TACACGATGATCCAGAGAGTGGCGGGCGCAACGTAAGTACCGCGGGTGGAGACTACCTG 240
241 TACACGATGATCCAGAGAGTGGCGGGCGCAACGTAAGTACCGCGGGTGGAGACTACCTG 240
241 TACACGATGATCCAGAGAGTGGCGGGCGCAACGTAAGTACCGCGGGTGGAGACTACCTG 240
301 CTGTGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
301 CTGTGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
361 GCGTCAAGTGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
361 GCGTCAAGTGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
421 ATCATTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
421 ATCATTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
481 AGGTTGCTGGAAGGCGCTTGTGTTAGATACCATTTGTTTATGCTTATGCTTATGCTTAT 540
481 AGGTTGCTGGAAGGCGCTTGTGTTAGATACCATTTGTTTATGCTTATGCTTATGCTTAT 540
541 GTTGTTCGCAAAAACCTCAGGTAATATTTTGGCAGTGGCAGTGGCAGTGGCAGTGGCAG 600
541 GTTGTTCGCAAAAACCTCAGGTAATATTTTGGCAGTGGCAGTGGCAGTGGCAGTGGCAG 600
601 TTCTCTACAGTCTCCGCAATGCTGCGATGATGATGATGATGATGATGATGATGATGATG 660
601 TTCTCTACAGTCTCCGCAATGCTGCGATGATGATGATGATGATGATGATGATGATGATG 660
661 GGTTCAGTGGTATATGCTCAGCAGCAAGGAATTAATCAAGCTTGTGATCATAGATTTTGG 720
661 GGTTCAGTGGTATATGCTCAGCAGCAAGGAATTAATCAAGCTTGTGATCATAGATTTTGG 720
721 GTTCTTATTTTTCGTTCTTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

721 GTTCTTATTTTTCGTTCTTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
781 TCTACATATGCAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
781 TCTACATATGCAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
841 GACAAACCTCCCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
841 GACAAACCTCCCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
901 ATTCTTTCTTTCGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
901 ATTCTTTCTTTCGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
961 GACACACACCGCGCAGAAACACTTTGAGAAAGAGAACCCAGCTCCCAACCTCATTCAG 1020
961 GACACACACCGCGCAGAAACACTTTGAGAAAGAGAACCCAGCTCCCAACCTCATTCAG 1020
1021 TGTGTTGGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
1021 TGTGTTGGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
1081 CACTTGAAGGCTTGCACACCTGACACCTTACCA----- 1115
1081 CACTTGAAGGCTTGCACACCTGACACCTTACCA----- 1115
1116 --TCAGAAAGCTAAGTTTTAAGAGAGGAGTGGCGATGCTGATGCTGACCGGCGAGATAT 1173
1116 --TCAGAAAGCTAAGTTTTAAGAGAGGAGTGGCGATGCTGATGCTGACCGGCGAGATAT 1173
1141 AGTCAGAAAGCTAAGTTTTAAGAGAGGAGTGGCGATGCTGATGCTGACCGGCGAGATAT 1200
1141 AGTCAGAAAGCTAAGTTTTAAGAGAGGAGTGGCGATGCTGATGCTGACCGGCGAGATAT 1200
1174 AAGAGCGCAGCAAGCCTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1233
1174 AAGAGCGCAGCAAGCCTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1233
1201 AAGAGCGCAGCAAGCCTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1260
1201 AAGAGCGCAGCAAGCCTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1260
1234 GCGAGTCCACCAAGAGTGCAGAGAGCTGAGCTTCAACGACCGAAGCCGCTTCCGGGCC 1293
1234 GCGAGTCCACCAAGAGTGCAGAGAGCTGAGCTTCAACGACCGAAGCCGCTTCCGGGCC 1293
1261 GCGAGTCCACCAAGAGTGCAGAGAGCTGAGCTTCAACGACCGAAGCCGCTTCCGGGCC 1320
1261 GCGAGTCCACCAAGAGTGCAGAGAGCTGAGCTTCAACGACCGAAGCCGCTTCCGGGCC 1320
1294 TCGCTGGCGCTCAAAAGTTCACAGCAAAACCATGATGATGCTGACACAGCCCTTGGC 1353
1294 TCGCTGGCGCTCAAAAGTTCACAGCAAAACCATGATGATGCTGACACAGCCCTTGGC 1353
1321 TCGCTGGCGCTCAAAAGTTCACAGCAAAACCATGATGATGCTGACACAGCCCTTGGC 1380
1321 TCGCTGGCGCTCAAAAGTTCACAGCAAAACCATGATGATGCTGACACAGCCCTTGGC 1380
1354 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1413
1354 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1413
1381 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
1381 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
1414 CCACCACTTAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1473
1414 CCACCACTTAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1473
1441 CCACCACTTAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
1441 CCACCACTTAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
1474 AAGTTTAAAGAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1533
1474 AAGTTTAAAGAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1533
1501 AAGTTTAAAGAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
1501 AAGTTTAAAGAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
1534 GGTTCATCTGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1593
1534 GGTTCATCTGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1593
1561 GGTTCATCTGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1561 GGTTCATCTGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1594 GGAAGAGGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1653
1594 GGAAGAGGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1653
1621 GGAAGAGGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1621 GGAAGAGGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1654 ACCACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1713
1654 ACCACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1713
1681 ACCACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
1681 ACCACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
1714 ATAGAGTCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1773
1714 ATAGAGTCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1773
1741 ATAGAGTCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
1741 ATAGAGTCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
1774 GCTTCAGCCCTGCTTGGCTTATCTGATGATGATGATGATGATGATGATGATGATGATG 1833
1774 GCTTCAGCCCTGCTTGGCTTATCTGATGATGATGATGATGATGATGATGATGATGATG 1833

| | | | |
|----------|---|--|------|
| Db | 1801 | GCCTAGGCCCTGGCTTTGGCTTCATTCCAGATCCACGCTTTTGGATGTGACAGACATCT | 1860 |
| Qy | 1834 | GACATATCAAGCCCTGTGGATGATGACAAGATCTTTTCGGTTTCGGCACAAAACAGTGGCTGC | 1893 |
| Db | 1861 | GACTATCAAGCCCTGTGGATGATGACAAGATCTTTTCGGTTTCGGCACAAAACAGTGGCTGC | 1920 |
| Qy | 1894 | TTATCCAGATCAACTAGTGTCCCAACATCTGTGAGAGGCCCTGCAGTTCAATTCTGAGCCCAAT | 1953 |
| Db | 1921 | TTATCCAGATCAACTAGTGTCCCAACATCTGTGAGAGGCCCTGCAGTTCAATTCTGAGCCCAAT | 1980 |
| Qy | 1954 | GAGTTCAGAGCCAGACTTTCTACGGCTTACGGGCTTACGCCCTACATATGACAGTCAAGCAACAG | 2013 |
| Db | 1981 | GAGTTCAGAGCCAGACTTTCTACGGGCTTACGGGCTTACGCCCTACATATGACAGTCAAGCAACAG | 2040 |
| Qy | 2014 | GTGCCAATTAGTCCAAAGCGATGGCTCAGCAGTGGCCAGCCACCAACATTACAGATCCACCTCTCCCA | 2073 |
| Db | 2041 | GTGCCAATTAGTCCAAAGCGATGGCTCAGCAGTGGCCAGCCACCAACATTACAGATCCACCTCTCCCA | 2100 |
| Qy | 2074 | ATTAATATGCGGACCCCAAGCGAGAGGCCCAACAAGTTTACAGATCCACCTCTCTCCCA | 2133 |
| Db | 2101 | ATTAATATGCGGACCCCAAGCGAGAGGCCCAACAAGTTTACAGATCCACCTCTCTCCCA | 2160 |
| Qy | 2134 | GCCATCAAGCATCTGCCCGAGGCCAGAAACTCTACCCCTAACCTCGACGCTTACAGGAA | 2193 |
| Db | 2161 | GCCATCAAGCATCTGCCCGAGGCCAGAAACTCTACCCCTAACCTCGACGCTTACAGGAA | 2220 |
| Qy | 2194 | AGCATTTTCAGACTCAACACCTGCTGTTGGCTCCCAAGGAAATGTTCAAGTTGCACAG | 2253 |
| Db | 2221 | AGCATTTTCAGACTCAACACCTGCTGTTGGCTCCCAAGGAAATGTTCAAGTTGCACAG | 2280 |
| Qy | 2254 | TCAAAATCTCACCAAGGACGTTCTATAGAGGAAAAAGCTTTGACATGGAGGAGAAACTCTG | 2313 |
| Db | 2281 | TCAAAATCTCACCAAGGACGTTCTATAGAGGAAAAAGCTTTGACATGGAGGAGAAACTCTG | 2340 |
| Qy | 2314 | TTGTCTGTCTGTCCCATGGTGGCCGAAGGACTTGGGCCAAATCTTTGTCTGTGCCAAACCTG | 2373 |
| Db | 2341 | TTGTCTGTCTGTCCCATGGTGGCCGAAGGACTTGGGCCAAATCTTTGTCTGTGCCAAACCTG | 2400 |
| Qy | 2374 | ATCAGGTGCAGCGAGGAAGTGAATATACAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA | 2433 |
| Db | 2401 | ATCAGGTGCAGCGAGGAAGTGAATATACAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA | 2460 |
| Qy | 2434 | GCGAGCCCAATTTTTCGCCCAATGGAGGGAATCCAAATGTTTATACATGATGAAGAG | 2493 |
| Db | 2461 | GCGAGCCCAATTTTTCGCCCAATGGAGGGAATCCAAATGTTTATACATGATGAAGAG | 2520 |
| Qy | 2494 | GTTGGGTCCCGAAGAGACAGACAGACACTTTTGATGCCGACCGCAGCCTGCACAGGAA | 2533 |
| Db | 2521 | GTTGGGTCCCGAAGAGACAGACAGACACTTTTGATGCCGACCGCAGCCTGCACAGGAA | 2580 |
| Qy | 2554 | GCTGCTTTTGCATCAGACTCTCTAAGGACGTGAAGTCAAGATCATCTCAAGCAATTTTGT | 2613 |
| Db | 2581 | GCTGCTTTTGCATCAGACTCTCTAAGGACGTGAAGTCAAGATCATCTCAAGCAATTTTGT | 2640 |
| Qy | 2614 | AAGCGAGAGAAAATACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAA 2667 | |
| Db | 2641 | AAGCGAGAGAAAATACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAA 2694 | |
| RESULT 6 | | | |
| AAS14651 | | | |
| ID | AAS14651 | standard; cDNA; 3071 BP. | |
| XX | | | |
| AC | AAS14651; | | |
| XX | | | |
| DT | 18-Dec-2001 (first entry) | | |
| XX | | | |
| DE | Human cDNA for voltage gated potassium channel hKvNO5. | | |
| XX | | | |
| KW | Human; ss: voltage-gated potassium channel; hKCNQ5; nontropic; | | |
| KW | cerebroprotective; neurotropic; analgesic; vision disorder; | | |
| KW | central nervous system disorder; epilepsy; migraine; hearing disorder | | |
| KW | psychotic disorder; seizure; learning disorder; memory disorder; | | |

KW stroke; pain; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 FE 20-MAR-2001; 2001WO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 XX
 DR WPI; 2001-611467/70.
 XX
 XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or
 PT membrane expressing the protein, comprises KCNQ alpha
 PT subunits - ,
 XX
 PS Claim 5; Page 61-62; 78pp; English.

The invention relates to an isolated polypeptide comprising an alpha-subunit of a KCNQ potassium channel, with a subsequence having 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence and forms a KCNQ potassium channel having the characteristic of voltage-gating with at least an additional KCNQ alpha-subunit. Also included in the scope of the invention are the nucleic acids encoding hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression vectors encoding them, antibodies against them, the use of 3-dimensional computer modelling to identify molecules that bind to a KCNQ containing potassium channel and modulate ion flux through the channel. The KCNQ polypeptide is useful for identifying a compound that increases or decreases ion flux through a potassium channel expressed in an eukaryotic host cell or cell membrane. The compound (and the KCNQ nucleic acid when used in gene therapy) is useful as a pharmaceutical agent for treating diseases involving abnormal ion flux such as disorders of the central nervous system, such as epilepsy, migraines, hearing and vision problems, psychotic disorders, seizures, learning and memory disorders, stroke and pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a human tissue and the use of a nucleotide sequence of KCNQ5 to search computer databases to find variants of the sequence which are associated with disease states, is useful for screening mutations of KCNQ5. The present sequence is a representative cDNA for hKCNQ5.

Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 1 other;

| | | | | |
|----------------------------|---------|---------------|--------|-------------------|
| Query Match | 98.5%; | Score 2626.4; | DB 22; | length 3071; |
| Best Local Similarity | 98.98%; | Pred. NO. 0; | | |
| Matches 2664; Conservative | 1; | Mismatches | 2; | Indels 27; Gaps 1 |

| | | | |
|----|-----|--|-----|
| QY | 1 | ATGAGAGATGTGGAGTGTGGGCGGAGAGGGTGTGCTGTAATCGGCAACCGCCAGAGGGG | 60 |
| Db | 10 | ATGAGAGATGTGGAGTGTGGGCGGAGAGGGTGTGCTGTAATCGGCAACCGCCAGAGGGG | 69 |
| QY | 61 | GACGCGCTGTCTACTGCTTGGGGCAACCGGCGCGGCTACACGCTTGGTGCGCGGCGGGGTGGCTTG | 120 |
| Db | 70 | GACGCGCTGTCTACTGCTTGGGGCAACCGGCGCGGCTACACGCTTGGTGCGCGGCGGGGTGGCTTG | 129 |
| QY | 121 | AGGAGAGAGCCCGCGGGGCAAGCAGAGGGGCGCCGCGATGAGCTCTGTGGGGAAGCGCTCTCT | 180 |
| Db | 130 | AGGAGAGAGCCCGCGGGGCAAGCAGAGGGGCGCCGCGATGAGCTCTGTGGGGAAGCGCTCTCT | 189 |
| QY | 181 | TACACGAGTACCCAGAGCTGTCCCGCGCAACGTCAGTACCGGCGGGGTGGAGACTACCTG | 240 |
| Db | 190 | TACACGAGTACCCAGAGCTGTCCCGCGCAACGTCAGTACCGGCGGGGTGGAGACTACCTG | 249 |
| QY | 241 | TACAACGTGCTGGAGAGACCCCGCGGTGGGCGTTATCTACCAACGCTTTCGTTTTTCTC | 300 |

Db 250 TACAACGTGCTGGAGAGAGACCCCGGCGTGGGCGTCACTACCAACGCTTTGTTTTCTC 309
OY 301 CTGTGCTTTGGTGGCTGATTTTGTTCAGTCTTTTACCAATCCCTGACGACACAAATTTG 360
Db 310 CTGTGCTTTGGTGGCTGATTTTGTTCAGTCTTTTACCAATCCCTGACGACACAAATTTG 369
OY 361 GCGTCAGTGGCTGCTGTGATCCGCGAGTTGCTGATATTCGTCCTTTGGTTGGAGTTTC 420
Db 370 GCGTCAGTGGCTGCTGTGATCCGCGAGTTGCTGATATTCGTCCTTTGGTTGGAGTTTC 429
OY 421 ATCATTTGGAATCTGCTGTCGCGGCTTCTGTTGCTATATAGAGANTGGCAAGAACTG 480
Db 430 ATCATTTGGAATCTGCTGTCGCGGCTTCTGTTGCTATATAGAGANTGGCAAGAACTG 489
OY 481 AGGTTTGGCTGGAAGCGCTTCGTGTATATAGATACCAATGCTTCTTATCGGTCATATGCA 540
Db 490 AGGTTTGGCTGGAAGCGCTTCGTGTATATAGATACCAATGCTTCTTATCGGTCATATGCA 549
OY 541 GTTGTGTTTGCAGAAAAGTCAAGGGTAATATTTTGGCAGCTCTGCACTCAGAAAGTCCCGT 600
Db 550 GTTGTGTTTGCAGAAAAGTCAAGGGTAATATTTTGGCAGCTCTGCACTCAGAAAGTCCCGT 609
OY 601 TTCTACAGATCTCTCCGATGTTGGCATGACCGGAAGGGAGGCACTTTGGAATTTACTG 660
Db 610 TTCTACAGATCTCTCCGATGTTGGCATGACCGGAAGGGAGGCACTTTGGAATTTACTG 669
OY 661 GGTTCAGTGGTTATGCTCACAGCAAGGAATTAATCAGCTGGTGCATATGGAATTTTTCG 720
Db 670 GGTTCAGTGGTTATGCTCACAGCAAGGAATTAATCAGCTGGTGCATATGGAATTTTTCG 729
OY 721 GTTCTATTTTTCGTCCTTTCTTGTCTATCTGTTGAGAAAAGATGGCAATTAAGAGTTT 780
Db 730 GTTCTATTTTTCGTCCTTTCTTGTCTATCTGTTGAGAAAAGATGGCAATTAAGAGTTT 789
OY 781 TCTACATATGAGATGCTCTCTGTGTGGGCGACAATTTACATTGACAACTATTTGCTATGGA 840
Db 790 TCTACATATGAGATGCTCTCTGTGTGGGCGACAATTTACATTGACAACTATTTGCTATGGA 849
OY 841 GACAAAGTCCCTTAAGCTTGGTGGGAAGATGCTTCTGAGGCTTTGCACTCCTTGGC 900
Db 850 GACAAAGTCCCTTAAGCTTGGTGGGAAGATGCTTCTGAGGCTTTGCACTCCTTGGC 909
OY 901 ATTTCCTTTTTCGACTTCTCTGCGCGCAATTTGCTCAGGTTTTCATTAAGATACAA 960
Db 910 ATTTCCTTTTTCGACTTCTCTGCGCGCAATTTGCTCAGGTTTTCATTAAGATACAA 969
OY 961 GAACAAACCGCCGAGAAACACTTTGAGAAAAGAAAGAAACCCAGCTGCCAACCCTCATTTAG 1020
Db 970 GAACAAACCGCCGAGAAACACTTTGAGAAAAGAAAGAAACCCAGCTGCCAACCCTCATTTAG 1029
OY 1021 TGTGTTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA 1080
Db 1030 TGTGTTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA 1089
OY 1081 CACTTGAAGGCTTTGACACCTGACGCCCTACCA----- 1115
Db 1090 CACTTGAAGGCTTTGACACCTGACGCCCTACCA----- 1149
OY 1116 --TCAGAAAGTAAAGTTTAAGAGAGAGAGTGGCAATGCTTACGCCCCAGGGGCGAGAGTAT 1173
Db 1150 AGTCAGAGGCTAAAGTTTAAAGAGAGAGTGGCAATGCTTACGCCCCAGGGGCGAGAGTAT 1209
OY 1174 AAGAGCGCAAGAGCTCAGTAGGTGACAGAGAGGTCCCAAGACCGCAGATCAGACCGAG 1233
Db 1210 AAGAGCGCGAAGAGCTCAGTAGGTGACAGAGAGGTCCCAAGACCGCAGATCAGACCGAG 1269
OY 1234 GGCAGTCCCAAGAGTGCAGAAAGTGTGAGCTTCAACGACCGAAACCGGCTTCCGGGCC 1293
Db 1270 GGCAGTCCCAAGAGTGCAGAAAGTGTGAGCTTCAACGACCGAAACCGGCTTCCGGGCC 1329
OY 1294 TCGGTGGGCGCAAAAGTTCACAGCAAAACAGATAGATGTGACACAGACCCCTTTGGC 1353
Db 1330 TCGGTGGGCGCAAAAGTTCACAGCAAAACAGATAGATGTGACACAGACCCCTTTGGC 1389

OY 1354 ACTGATGATGATATATGATGAAAAAGAGATCCAGTGTATGATCACTGGAGAACCTTCACC 1413
Db 1390 ACTGATGATGATATATGATGAAAAAGAGATCCAGTGTATGATCACTGGAGAACCTTCACC 1449
OY 1414 CCACCACTTAAAGTGTCACTTTGAGCTATGACAAATTTATGAAATTTTATGTTGCAAAAACGG 1473
Db 1450 CCACCACTTAAAGTGTCACTTTGAGCTATGACAAATTTATGAAATTTTATGTTGCAAAAACGG 1509
OY 1474 AAGTTTAAGGAAGCTTACGTGCATATGATGTTAAAGATGTCAATATTTTCGCT 1533
Db 1510 AAGTTTAAGGAAGCTTACGTGCATATGATGTTAAAGATGTCAATATTTTCGCT 1569
OY 1534 GGTCACTTGGACATGTTGTTAGAAATTTAAAGCCTTCAACACGCTTGTGCAAAATTCCT 1593
Db 1570 GGTCACTTGGACATGTTGTTAGAAATTTAAAGCCTTCAACACGCTTGTGCAAAATTCCT 1629
OY 1594 GGAAGAGGCAAAATCAATCAATGATGAAGAGAGCGGAGAGAAAAATTAACGAGAACATGAG 1653
Db 1630 GGAAGAGGCAAAATCAATCAATGATGAAGAGAGCGGAGAGAAAAATTAACGAGAACATGAG 1689
OY 1654 ACCACAGAGATCTCAGTATGCTCGGTCGAGGTGCAAGGTTGAAAAACAGTACAGTCC 1713
Db 1690 ACCACAGAGATCTCAGTATGCTCGGTCGAGGTGCAAGGTTGAAAAACAGTACAGTCC 1749
OY 1714 ATGAGTCCCAAGCTGAGCTGACCTTACTAGACATCTATCAACAGGTCCTTGGAAAGGCTCT 1773
Db 1750 ATGAGATCCCAAGCTGAGCTGACCTTACTAGACATCTATCAACAGGTCCTTGGAAAGGCTCT 1809
OY 1774 GCTTCAGCCCTGCTTTGGCTTCTATTCAGATTCACACCTTTTGAATGTGAACAGACATCT 1833
Db 1810 GCTTCAGCCCTGCTTTGGCTTCTATTCAGATTCACACCTTTTGAATGTGAACAGACATCT 1869
OY 1834 GACTATCAAGCCCTGCTGATACCAAGATCTTGGGTTCCCGCACAAAACAGTGGCTGC 1893
Db 1870 GACTATCAAGCCCTGCTGATACCAAGATCTTGGGTTCCCGCACAAAACAGTGGCTGC 1929
OY 1894 TTATCCAGATCAATGATGCGCAACATCTCGAAGAGCCCTGCAATTTCTGACGCCAAAT 1953
Db 1930 TTATCCAGATCAATGATGCGCAACATCTCGAAGAGCCCTGCAATTTCTGACGCCAAAT 1989
OY 1954 GAGTTAGGCGCCAGACTTCTACGCGCTTAAAGCCTTATGCAAGTCAAGCAAGACAG 2013
Db 1990 GAGTTAGGCGCCAGACTTCTACGCGCTTAAAGCCTTATGCAAGTCAAGCAAGACAG 2049
OY 2014 GTGCCAATTAGTCAAAAGCGATGCTCAGCAGTGGGCAAGCCCAACACCATTTGCAACCAA 2073
Db 2050 GTGCCAATTAGTCAAAAGCGATGCTCAGCAGTGGGCAAGCCCAACACCATTTGCAACCAA 2109
OY 2074 ATTAATACGGCACCCAAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2133
Db 2110 ATTAATACGGCACCCAAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2169
OY 2134 GGCATCAAGATCTGCGCCAGGCGAGAAAGCTGCAACCTTAACCTGCAAGGCTTACAGGAA 2193
Db 2170 GGCATCAAGATCTGCGCCAGGCGAGAAAGCTGCAACCTTAACCTGCAAGGCTTACAGGAA 2229
OY 2194 AGCATTTCTGACGTCACACACCTGCTTGTTCCTCCCAAGGAAATTTGTCAGTTGACAG 2253
Db 2230 AGCATTTCTGACGTCACACACCTGCTTGTTCCTCCCAAGGAAATTTGTCAGTTGACAG 2289
OY 2254 TCAAAATCTCAACAAAGAGCGCTTCTATGAGAAAAAGCTTTGACATGGGAGGAAAACTGTG 2313
Db 2290 TCAAAATCTCAACAAAGAGCGCTTCTATGAGAAAAAGCTTTGACATGGGAGGAAAACTGTG 2349
OY 2314 TTGTCTGTTCTGCTCCATGAGTGGCCGAAGACTTGGGCAAAATTTTGTCTGTGCAAAAACCTG 2373
Db 2350 TTGTCTGTTCTGCTCCATGAGTGGCCGAAGACTTGGGCAAAATTTTGTCTGTGCAAAAACCTG 2409
OY 2374 ATCAGGTGCAACCGAGAACTGAATATACAACTTTCAGGAGTGAATCAAGTGGCTCCAGA 2433
Db 2410 ATCAGGTGCAACCGAGAACTGAATATACAACTTTCAGGAGTGAATCAAGTGGCTCCAGA 2469

XX 21-MAR-2000; 2000DE-1013732.
PF 21-MAR-2000; 2000DE-1013732.
XX 21-MAR-2000; 2000DE-1013732.
XX (AVET) AVENTIS PHARMA DEUT GMBH.
PI Steilmeyer K, Lerche C, Scherer C, Seebold G, Busch AE;
XX WPI; 2001-571700/65.
DR P-PSDB; AAB86979.
XX
XX New DNA sequence encoding potassium channel KCNQ5, useful in screening
PT for specific modulators, potential agents for treating central nervous
PT system and cardiovascular diseases
PS
PS Claim 2a; Page 9-10; 20pp; German.
XX
XX This invention describes a novel DNA sequence (I) encoding: (i) a
CC polypeptide (II) with potassium channel KCNQ5 activity; (ii) a
CC polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
CC the invention have neurological, cardiovascular and anticonvulsant
CC activity and act as modulators of the voltage-dependent KCNQ5 potassium
CC channel, a key regulator of membrane potential and modulator of
CC excitability of electrically activated cells such as neurons and
CC cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
CC are used to screen for compounds that modulate the activity of KCNQ5,
CC potentially useful for treating central nervous system (e.g. epilepsy),
CC and cardiovascular diseases. This sequence encodes the human
CC potassium channel KCNQ5 protein described in the invention.
XX
SQ Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 other:

Query Match 98.1%; Score 2617.2; DB 22; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;

QY 1 ATGAAGATGTCGATCGGCGGCGGAGAGTGTCTGTAACGCGGAGCGGCGGAGGCG 60
DB 215 ATGAAGATGTCGATCGGCGGCGGAGAGTGTCTGTAACGCGGAGCGGCGGAGGCG 274
QY 61 GAGCGCTGCTACTGCTGGGACCGCGCGGCGGAGCGGCGGCGGCGGCGGCGGCTG 120
DB 275 GAGCGCTGCTACTGCTGGGACCGCGCGGCGGAGCGGCGGCGGCGGCGGCGGCTG 334
QY 121 AGGAGACCGCGGCGGAGAGGCGGCGGAGTGTCTGTAACGCGGAGCGGCGGCTGCT 180
DB 335 AGGAGACCGCGGCGGAGAGGCGGCGGAGTGTCTGTAACGCGGAGCGGCGGCTGCT 394
QY 181 TACAGAGTACGAGAGTGTCTGCGGCGGAGTGTCTGTAACGCGGAGCGGCGGAGTGTCTG 240
DB 395 TACAGAGTACGAGAGTGTCTGCGGCGGAGTGTCTGTAACGCGGAGCGGCGGAGTGTCTG 454
QY 241 TACAGAGTGTCTGAGAGAGCGGCGGCGGAGTGTCTGTAACGCGGAGCGGCGGAGTGTCTG 300
DB 455 TACAGAGTGTCTGAGAGAGCGGCGGCGGAGTGTCTGTAACGCGGAGCGGCGGAGTGTCTG 514
QY 301 CTGTGCTTGTGCTGTGATTTTGTACGTTTGTACCATCCCTTGTAGACACAAATTTG 360
DB 515 CTGTGCTTGTGCTGTGATTTTGTACGTTTGTACCATCCCTTGTAGACACAAATTTG 574
QY 361 GCGTCAAGTGTGCTGTGATTTTGTAGTGTGATTTGTGATTTGTGATTTGTGATTTG 420
DB 575 GCGTCAAGTGTGCTGTGATTTTGTAGTGTGATTTGTGATTTGTGATTTGTGATTTG 634
QY 421 ATCATTCGATTCGTGTGCGGCTGTGCTGTGATTCGATTCGATTCGATTCGATTCG 480
DB 635 ATCATTCGATTCGTGTGCGGCTGTGCTGTGATTCGATTCGATTCGATTCGATTCG 694
QY 481 AGTTTGTGCTGGAAGCCCTTGTGTGTATAGATACCATTTGTATCGTTTAAATAGCA 540
DB 695 AGTTTGTGCTGGAAGCCCTTGTGTGTATAGATACCATTTGTATCGTTTAAATAGCA 754

QY 541 GTTGTTCGCAAAAGCTCAGGCTAATATTTTGGACGCTGCGACGTCAGAGTCTCCGT 600
DB 755 GTTGTTCGCAAAAGCTCAGGCTAATATTTTGGACGCTGCGACGTCAGAGTCTCCGT 814
QY 601 TTCTTACAGATCTCCGATGCTGCGGAGTGGAGCGGAGGAGGAGGAGTGGAAATTTAGTG 660
DB 815 TTCTTACAGATCTCCGATGCTGCGGAGTGGAGCGGAGGAGGAGGAGTGGAAATTTAGTG 874
QY 661 GGTTCAGTGTGTTATGTCACAGCAAGCAATTAATACACGCTTGTACATAGATTTTGG 720
DB 875 GGTTCAGTGTGTTATGTCACAGCAAGCAATTAATACACGCTTGTACATAGATTTTGG 934
QY 721 GTTCTTATTTTGTGCTTCTTCTGCTATCTGCTGGAAGGAGGAGGAGGAGGAGTGT 780
DB 935 GTTCTTATTTTGTGCTTCTTCTGCTATCTGCTGGAAGGAGGAGGAGGAGGAGTGT 994
QY 781 TCTACATATGAGATGCTCTGCTGCTGGGAGCAATTTACATTTGACATTTGCTATGCA 840
DB 995 TCTACATATGAGATGCTCTGCTGCTGGGAGCAATTTACATTTGACATTTGCTATGCA 1054
QY 841 GACAAAGTCCCTTAACTTGGCTGGGAAGATTTGCTTTCGACGCTTTCGACTCCTTGGC 900
DB 1055 GACAAAGTCCCTTAACTTGGCTGGGAAGATTTGCTTTCGACGCTTTCGACTCCTTGGC 1114
QY 901 ATTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 1115 ATTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1174
QY 961 GAAACACAGCGCGGAGAAACACTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1020
DB 1175 GAAACACAGCGCGGAGAAACACTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1234
QY 1021 TGTGTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1235 TGTGTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1294
QY 1081 CACTTGAAGGCTTGCACACCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTG 1115
DB 1295 CACTTGAAGGCTTGCACACCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTG 1354
QY 1116 --TCGAGAGCTAAGTTTAAAGAGCGAGTGGCTAGCGCTAGCGCTAGCGCTAGCGCT 1173
DB 1355 AGTCAAGAGCTAAGTTTAAAGAGCGAGTGGCTAGCGCTAGCGCTAGCGCTAGCGCTAG 1414
QY 1174 AAGAGCGGACAGGCTGAGTGTGAGAGAGGCTCCCAAGCAGCAGCAGCAGCAGCAGCAG 1233
DB 1415 AAGAGCGGACAGGCTGAGTGTGAGAGAGGCTCCCAAGCAGCAGCAGCAGCAGCAGCAG 1474
QY 1234 GGCAGTCCCAAGAGTGCAGAGAGGCTGAGGCTTCAACGAGCAGCAGCAGCAGCAGCAG 1293
DB 1475 GGCAGTCCCAAGAGTGCAGAGAGGCTGAGGCTTCAACGAGCAGCAGCAGCAGCAGCAG 1534
QY 1294 TCGCTGCGCTCAAAAGTTCACGCAAAACAGTGTATGATGCTGACACAGCCTTGGC 1353
DB 1535 TCGCTGCGCTCAAAAGTTCACGCAAAACAGTGTATGATGCTGACACAGCCTTGGC 1594
QY 1354 ACTGATGATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
DB 1595 ACTGATGATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1654
QY 1414 CCACACCTTAAAGCTGATTCGAGCTATCAGAAATTTATGAAATTTTCAATGTTGCAAAAGCG 1473
DB 1555 CCACACCTTAAAGCTGATTCGAGCTATCAGAAATTTATGAAATTTTCAATGTTGCAAAAGCG 1714
QY 1474 AAGTTTAAAGAAAGTTCATGCTATGATGATGATGATGATGATGATGATGATGATGAT 1533
DB 1715 AAGTTTAAAGAAAGTTCATGCTATGATGATGATGATGATGATGATGATGATGATGAT 1774
QY 1534 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1593
DB 1775 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1834
QY 1594 GGAAGAGGCGCAATACATCAGATTAAGAGAGCGGAGAGAAATTAACAGCAGACATGAG 1653

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Db 1835 GGAAGAGGCAATCATCATCATATAGAAAGAGCCGAGAGAAATATACAGACGAAATGAG 1894
      |||
Qy 1654 ACCAGAGAGATCTAGATATGCTGGTGGTGTCAAGTGTGAAAAACAGTACAGTCC 1713
      |||
Db 1895 ACCAGAGAGATCTAGATATGCTGGTGGTGTCAAGTGTGAAAAACAGTACAGTCC 1954
      |||
Qy 1714 ATAGAGTCCAACTGGAGTGGCTACTAGACATCTATCAACAGTCCCTTGGGAAAGGCTCT 1773
      |||
Db 1955 ATAGATCCAACTGGAGTGGCTACTAGACATCTATCAACAGTCCCTTGGGAAAGGCTCT 2014
      |||
Qy 1774 GCGTACGCGCTGGCTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT 1833
      |||
Db 2015 GCGTACGCGCTGGCTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT 2074
      |||
Qy 1834 GACTATCAAGCCCTGTGATACCAAGATCTTTCGGGTCCGACAAAACAGTGGCTGC 1893
      |||
Db 2075 GACTATCAAGCCCTGTGATACCAAGATCTTTCGGGTCCGACAAAACAGTGGCTGC 2134
      |||
Qy 1894 TTATCCAGATCAACTGATGTCGACATCTGAGAGGCTGACATTCATTCGAGCCCAAT 1953
      |||
Db 2135 TTATCCAGATCAACTGATGTCGACATCTGAGAGGCTGACATTCATTCGAGCCCAAT 2194
      |||
Qy 1954 GAGTTCAGTCCAGACTTTCAGGCGCTTACGCTTACTATGACAGTCAAGCAACACAG 2013
      |||
Db 2195 GAGTTCAGTCCAGACTTTCAGGCGCTTACGCTTACTATGACAGTCAAGCAACACAG 2254
      |||
Qy 2014 GTGCCAATTAATGTCGAGTGGTCAAGAGTGGAGCCACCAACACATTCGAAACCAA 2073
      |||
Db 2255 GTGCCAATTAATGTCGAGTGGTCAAGAGTGGAGCCACCAACACATTCGAAACCAA 2314
      |||
Qy 2074 ATAAATAGGAGGACCCAGAGGAGGAGCCCAACAACTTACAGATCCACGCTCTCCCA 2133
      |||
Db 2315 ATAAATAGGAGGACCCAGAGGAGGAGCCCAACAACTTACAGATCCACGCTCTCCCA 2374
      |||
Qy 2134 GGCATCAAGCATCTGCCAGGAGCCAGAAACTCTGCACCTTAACCTTGAGAGCTTACAGAA 2193
      |||
Db 2375 GGCATCAAGCATCTGCCAGGAGCCAGAAACTCTGCACCTTAACCTTGAGAGCTTACAGAA 2434
      |||
Qy 2194 AGCATTTCTGACGTCACACCTGCTTGTGCTCCAGAGAAATGTTACAGTTCACAG 2253
      |||
Db 2435 AGCATTTCTGACGTCACACCTGCTTGTGCTCCAGAGAAATGTTACAGTTCACAG 2494
      |||
Qy 2254 TCNAATCTCAGCAGAGACGCTTCTATGAGAAAGCTTGAATGAGAGAGAGAAACTGTG 2313
      |||
Db 2495 TCNAATCTCAGCAGAGACGCTTCTATGAGAAAGCTTGAATGAGAGAGAGAAACTGTG 2554
      |||
Qy 2314 TTGTCGTCTGTCATGATGTCGCGAAGGACTTGGCAAAATCTTGTGTGCAAAACCTG 2373
      |||
Db 2555 TTGTCGTCTGTCATGATGTCGCGAAGGACTTGGCAAAATCTTGTGTGCAAAACCTG 2614
      |||
Qy 2374 ATCAGGTTCAGCAGAGACGATGATATCAACTTTCAGGAGATGATGATGAGGCTCCGA 2433
      |||
Db 2615 ATCAGGTTCAGCAGAGACGATGATATCAACTTTCAGGAGATGATGATGAGGCTCCGA 2674
      |||
Qy 2434 GGCAGCAGAGATTTTATCCCAATGAGAGGAATCCAAATTTGTTATTAACGATGAAGAG 2493
      |||
Db 2675 GGCAGCAGAGATTTTATCCCAATGAGAGGAATCCAAATTTGTTATTAACGATGAAGAG 2734
      |||
Qy 2494 GTGGGTCCGAGAGACAGACAGACACATTTTGTATGCCGACCGCAGCCTGCGCAGGAA 2553
      |||
Db 2735 GTGGGTCCGAGAGAGAGAGACAGACATTTTGTATGCCGACCGCAGCCTGCGCAGGAA 2794
      |||
Qy 2554 GTGGGTCCGAGACATCTCTTAAGAGCTGGAAGGTGACATATCTCAAGAGCATTTTGT 2613
      |||
Db 2795 GTGGGTCCGAGACATCTCTTAAGAGCTGGAAGGTGACATATCTCAAGAGCATTTTGT 2854
      |||
Qy 2614 AAGGAGAGAGAGATACAGATGAGTGGCTTACGCTTGCCTCATGTCAAACTGAATTA 2667
      |||
Db 2855 AAGGAGAGAGAGATACAGATGAGTGGCTTACGCTTGCCTCATGTCAAACTGAATTA 2908
      |||

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AAC64371
ID AAC64371 standard. cDNA: 3718 BP.
AC
AC AAC64371;
DT 07-FEB-2001 (first entry)
XX
DE Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
XX
KW Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW Salla disease; ophthalmological; auditory; central nervous system;
KW cardioactive; anticonvulsant; gastrointestinal; muscular active;
KW age-related neuronal degeneration; macular degeneration; deafness;
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW gastrointestinal disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200061606-A1.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US09587.
XX
PR 14-APR-1999; 99US-0129274.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Petrukhin K, Caskey CT, Li W, Metzker ML;
XX
DR WPI: 2000-647417/62.
XX
DR P-PSDB: AAB24241.
XX
PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT inhibitors and activators which can treat e.g. Stargardt-like macular
PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
XX
PS Claim 3; Fig 2; 99p; English.
XX
CC The present sequence encodes the human KCNQ5 (also called KCN6q)
CC protein, which is a voltage-gated potassium channel protein. Human
CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
CC cardioactive, anticonvulsant, gastrointestinal and muscular active
CC activities. Sequences and methods from the present invention are useful
CC for identifying activators or inhibitors of KCNQ5 protein. These
CC activators and inhibitors are useful for treating Stargardt-like macular
CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
CC degeneration, other forms of macular degeneration, deafness, epilepsy,
CC and different forms of neuropsychiatric, heart, gastrointestinal, and
CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
CC dystrophies are located at chromosome 6q.
XX
SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 other;
XX
Query Match 94.5%; Score 2521; DB 21; Length 3718;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2564; Conservative 0; Mismatches 10; Indels 27; Gaps 1;
Qy 94 ACGCTTGTGGCGCGGCGGTGGCTGAGGAGAGCCCGGGGCAAGAGGGGCGCCG 153
      |||
Db 78 ACTGCTGAGGAGACTGCGCGGTGGCTGAGGAGAGAGCCCGGGGCAAGAGGGGCGCCG 137
      |||
Qy 154 ATGAGCTGCTGGGGAAGCGCTCTTACAGAGATGAGCAGAGCTCCGCGCAACGTC 213
      |||
Db 138 ATGAGCTGCTGGGGAAGCGCTCTTACAGAGATGAGCAGAGCTCCGCGCAACGTC 197
      |||
Qy 214 AAGTACGCGCGGTGAGAGACTACTGTACAACTGCTGAGAGAGACCCGCGGCTGGGCG 273
      |||
Db 198 AAGTACGCGCGGTGAGAGACTACTGTACAACTGCTGAGAGAGACCCGCGGCTGGGCG 257
      |||
Qy 274 TTCATCTACACGCTTTCGTTTTCCTCTTGTGCTTGGCTTGAATTTTGTACGTGTTT 333
      |||

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Db 258 TTCACTACACAGGCTTGGTTTCTCCTTGTGTTGGTTGATTTTGTCAAGTTT 317
QY 334 TCTACCATCCCTGAGACACACAAATTTGGCCTCAAGTGGCTCTGTGTTCTGGAGTTCTG 393
Db 318 TCTACCATCCCTGAGACACACAAATTTGGCCTCAAGTGGCTCTGTGATCCCTGGAGTTCTG 377
QY 394 ATGATTTGCTGTTGGTTGGATTTGATCATTTGCAATCTGGTCTGCGGTTGCTGTGT 453
Db 378 ATGATTTGCTGTTGGTTGGATTTGATCATTTGCAATCTGGTCTGCGGTTGCTGTGT 437
QY 454 CGATATAGAGATGGCAAGAGAGACTGAGTTTGTCTGCAAGCCCTCTGTGTTATAGAT 513
Db 438 CGATATAGAGATGGCAAGAGAGACTGAGTTTGTCTGCAAGCCCTCTGTGTTATAGAT 497
QY 514 ACCATTTGTTATGCGTTTCATATAGCAGTTGTTTCTGCAAAAACTAGGGTAAATATTTT 573
Db 498 ACCATTTGTTATGCGTTTCATATAGCAGTTGTTTCTGCAAAAACTAGGGTAAATATTTT 557
QY 574 GCCACGTCGACCTCAGAGTCTCCGTTTCTTACAGATCCCTCGCATGGTGGCATGGAC 633
Db 558 GCCACGTCGACCTCAGAGTCTCCGTTTCTTACAGATCCCTCGCATGGTGGCATGGAC 617
QY 634 CGAAGGGAGGCACTTGGAAATTTACTGGGTTAGTGGTTATGCTCACAAGCAAGAAATTA 693
Db 618 CGAAGGGAGGCACTTGGAAATTTACTGGGTTAGTGGTTATGCTCACAAGCAAGAAATTA 677
QY 694 ATCAAGCTTGTACATAGATTTTGGTCTTATTTTGGCTTCTGCTGTCTATCTG 753
Db 678 ATCAAGCTTGTACATAGATTTTGGTCTTATTTTGGCTTCTGCTGTCTATCTG 737
QY 754 GTGAAAAAGATGCCAATAAGAGTTTCTACATATGAGATGCTCTGTGGGGCACA 813
Db 738 GTGAAAAAGATGCCAATAAGAGTTTCTACATATGAGATGCTCTGTGGGGCACA 797
QY 814 ATTACATTTGAACATATTGGCTATGAGACAAAACTCCCTTACTTGGCTGGAGATTG 873
Db 798 ATTACATTTGAACATATTGGCTATGAGACAAAACTCCCTTACTTGGCTGGAGATTG 857
QY 874 CTTTCTCAGAGCTTTCGACCTCCTTGGCACTTCTTCTTGGCACTTCTGCGGCACTTCT 933
Db 858 CTTTCTCAGAGCTTTCGACCTCCTTGGCACTTCTTCTTGGCACTTCTGCGGCACTTCT 917
QY 934 GCGTCAGGTTTTCATTAAAGTACAGAACACACCGCCAGAAAACATTTGAGAAAAGA 993
Db 918 GCGTCAGGTTTTCATTAAAGTACAGAACACACCGCCAGAAAACATTTGAGAAAAGA 977
QY 994 AGGAACCCAGCTGCAACCTCATTCAGTGTGTTGGCGTATGAGCAGCTATGAGAA 1053
Db 978 AGGAACCCAGCTGCAACCTCATTCAGTGTGTTGGCGTATGAGCAGCTATGAGAA 1037
QY 1054 TCTGTTTCATTGCACTGGAAGGCACTTGAAGGCTTGCACACCGCAGCCCTTACC 1113
Db 1038 TCTGTTTCATTGCACTGGAAGGCACTTGAAGGCTTGCACACCGCAGCCCTTACC 1097
QY 1114 AA-----TCAGAGCTAAGTTTAAAGAGGAGATGCGC 1146
Db 1098 AAGAAAAGAACAGGGGAAGCATCAAGCAGTCAGAGCTAAGTTTAAAGAGGAGATGCGC 1157
QY 1147 ATGGCTAGCCCCAGGGGCGAAGTATTAAGAGCCGACAAGCCTCAGTAGTACAGAGAG 1206
Db 1158 ATGGCTAGCCCCAGGGGCGAAGTATTAAGAGCCGACAAGCCTCAGTAGTACAGAGAG 1217
QY 1207 TCCCAAGCACGCAATCACAGCGAGGGAGTCCACCAAAAGTCCAGAGAGAGTGGAGC 1266
Db 1218 TCCCAAGCACGCAATCACAGCGAGGGAGTCCACCAAAAGTCCAGAGAGAGTGGAGC 1277
QY 1267 TTCACAGACGAAACCCGCTTCCGGCCCTCGCTGCGCTCAAAAAGTTCTCAGCCAAACCA 1326
Db 1278 TTCACAGACGAAACCCGCTTCCGGCCCTCGCTGCGCTCAAAAAGTTCTCAGCCAAACCA 1337
QY 1327 GTGATAGATGCTGACACAGCCCTTGGCAGCTATGATGTATATGATGAAAAGAGATGCCAG 1386
Db 1338 GTGATAGATGCTGACACAGCCCTTGGCAGCTATGATGTATATGATGAAAAGAGATGCCAG 1397
QY 1387 TGTGATGATGAGTGAAGAGACCTACCCACACCTTAAAACTGTCACTTGGAGCTATGACA 1446
Db 1398 TGTGATGATGAGTGAAGAGACCTACCCACACCTTAAAACTGTCACTTGGAGCTATGACA 1457
QY 1447 ATTATGAATTTGATGTTGCAAAACGGAGTTTAAAGAAAGTTTACGTCGATATGATGA 1506
Db 1458 ATTATGAATTTGATGTTGCAAAACGGAGTTTAAAGAAAGTTTACGTCGATATGATGA 1517
QY 1507 AAAGATGTCATTTGAACATATTTCTGCTGTCATCTGACATGTTGTTGATTAATTAAGC 1566
Db 1518 AAAGATGTCATTTGAACATATTTCTGCTGTCATCTGACATGTTGTTGATTAATTAAGC 1577
QY 1567 CTTTCAACACGCTGTGATCAAAATCTTGGAAAAGGGCAAAATCACATCAGATTAAGAGAC 1626
Db 1578 CTTTCAACACGCTGTGATCAAAATCTTGGAAAAGGGCAAAATCACATCAGATTAAGAGAC 1637
QY 1627 CGAGAGAAATTAACAGAGACATGAGACACAGACATCTCAGATATGCTGGTGGGGTG 1686
Db 1638 CGAGAGAAATTAACAGAGACATGAGACACAGACATCTCAGATATGCTGGTGGGGTG 1697
QY 1687 GTCAAGTTGAAAAACAGGTACAGTCCATGAGATCCAAAGCTGGAGCTGCTACTAGACATC 1746
Db 1698 GTCAAGTTGAAAAACAGGTACAGTCCATGAGATCCAAAGCTGGAGCTGCTACTAGACATC 1757
QY 1747 TATCAACAGGCTTGGGAAAAGGCTTCCCTCAGCCCTCGCTTGGCTTCAATTCAGATC 1806
Db 1758 TATCAACAGGCTTGGGAAAAGGCTTCCCTCAGCCCTCGCTTGGCTTCAATTCAGATC 1817
QY 1807 CCACCTTTTGAATGTGAACAGACATCTGACATCAAGCCCTGTGGATAGCAAAAGATCTT 1866
Db 1818 CCACCTTTTGAATGTGAACAGACATCTGACATCAAGCCCTGTGGATAGCAAAAGATCTT 1877
QY 1867 TCGGTTTCCGACAAAACAGTGGCTCTTATCAAGATCACTAGTGGCAACATCTGAGA 1926
Db 1878 TCGGTTTCCGACAAAACAGTGGCTCTTATCAAGATCACTAGTGGCAACATCTGAGA 1937
QY 1927 GGCCTGAGTTCAATTCGACGCGCAAAATGAGTTTCAAGTGGCCGACCTTCTAGCGGCTTAC 1986
Db 1938 GGCCTGAGTTCAATTCGACGCGCAAAATGAGTTTCAAGTGGCCGACCTTCTAGCGGCTTAC 1997
QY 1987 CCTACTATGACAGTCAAGACACAGAGTGGCAATTAAGTCAAGCGATGAGCTCAGCAGT 2046
Db 1998 CCTACTATGACAGTCAAGACACAGAGTGGCAATTAAGTCAAGCGATGAGCTCAGCAGT 2057
QY 2047 GCAGCCACCAACACATTTGCAAAACCAATTAATTAAGTGGCCAGCCAGCCCAACA 2106
Db 2058 GCAGCCACCAACACATTTGCAAAACCAATTAATTAAGTGGCCAGCCAGCCCAACA 2117
QY 2107 ACTTTACAGATCCACCTCTCTCCGAGCCATCAAGATCTGCGCAGGCGCAAAACCTGT 2166
Db 2118 ACTTTACAGATCCACCTCTCTCCGAGCCATCAAGATCTGCGCAGGCGCAAAACCTGT 2177
QY 2167 CACCTTAACCCCTCAGGCTTACAGAGAAAGCATTTCTACAGTCAACACCTGCTTGTGSC 2226
Db 2178 CACCTTAACCCCTCAGGCTTACAGAGAAAGCATTTCTACAGTCAACACCTGCTTGTGSC 2237
QY 2227 TCCAGGAAATATGTTAGGTTGCAACATCAAAATCTCACCAAGACCGTTCTATAGAGAA 2286
Db 2238 TCCAGGAAATATGTTAGGTTGCAACATCAAAATCTCACCAAGACCGTTCTATAGAGAA 2297
QY 2287 AGCTTGAACATGGGAGAGAAACCTGTTGCTGTCTGCTCCATGGTGGCGAAGAGACTG 2346
Db 2298 AGCTTGAACATGGGAGAGAAACCTGTTGCTGTCTGCTCCATGGTGGCGAAGAGACTG 2357
QY 2347 GGCAAATCTTTTGTCTGCAAAAACCTGATCAGTCCAGCCAGAACATGAATATCAACTT 2406
Db 2358 GGCAAATCTTTTGTCTGCAAAAACCTGATCAGTCCAGCCAGAACATGAATATCAACTT 2417
QY 2407 TCAGGAGTGAAGTCAAGTGGCTCCAGAGGACCAAGATTTTACCCCAATGAGAGGAA 2466
Db 2418 TCAGGAGTGAAGTCAAGTGGCTCCAGAGGACCAAGATTTTACCCCAATGAGAGGAA 2477

| | | | |
|-----------|--|---|------|
| QY | 2467 | TCGAAATGTTTATTAACGATGACAGAGGGGCTCCCGAAGAGACACAGACACGACTTTT | 2526 |
| | | | |
| Db | 2478 | TCGAAATGTTTATTAACGATGACAGAGGGGCTCCCGAAGAGACAGACAGACACTTTT | 2537 |
| QY | 2527 | GATGCCGACCGACACCCCTGCCAGGGAAGCTGCTTTGCATCAGACTCTTAAGGACTGGA | 2586 |
| | | | |
| Db | 2538 | GATGCCGACCGACACCCCTGCCAGGGAAGCTGCTTTGCATCAGACTCTTAAGGACTGGA | 2597 |
| QY | 2587 | AGGTCAGCATCTCOCAGACATTTGTGAAGCAGAGAAAGTACAGATGCCCTCAGCTTG | 2646 |
| | | | |
| Db | 2598 | AGGTCAGCATCTCOCAGACATTTGTGAAGCAGAGAAAGTACAGATGCCCTCAGCTTG | 2657 |
| QY | 2647 | CCTCATGTCAAACTGAATAA 2667 | |
| | | | |
| Db | 2658 | CCTCATGTCAAACTGAATAA 2678 | |
| RESULT 10 | | | |
| XX | AAC64370 | AAC64370 standard; DNA; 125910 BP. | |
| XX | AAC64370: | | |
| DT | 07-FEB-2001 | (first entry) | |
| XX | | | |
| DE | Human KCNQ5 (KCN6q) gene sequence SEQ ID NO:1. | | |
| XX | | | |
| KW | Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel; | | |
| KW | Stargardt-like macular dystrophy; cone-rod macular dystrophy; | | |
| KW | Salla disease; ophthalmological; auditory; central nervous system; | | |
| KW | cardioactive; anticonvulsant; gastrointestinal; muscular active; | | |
| KW | age-related macular degeneration; macular degeneration; deafness; | | |
| KW | epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder; | | |
| KW | gastrointestinal disorder; ds. | | |
| XX | | | |
| OS | Homo sapiens. | | |
| PN | WO200061606-A1. | | |
| XX | | | |
| PD | 19-OCT-2000. | | |
| XX | | | |
| PF | 10-APR-2000; 2000WO-US09587. | | |
| XX | | | |
| PR | 14-APR-1999; 99US-0129274. | | |
| XX | | | |
| PA | (MERI) MERCK & CO INC. | | |
| XX | | | |
| PI | Petrukhin K, Caskey CT, Li W, Metzker ML; | | |
| XX | | | |
| DR | WPI: 2000-647417/62. | | |
| XX | | | |
| PS | P-PSDB: AAB24241. | | |
| XX | | | |
| PT | Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying | | |
| PT | inhibitors and activators which can treat e.g. Stargardt-like macular | | |
| PT | dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy - | | |
| XX | Claim 3; Fig 1; 99pp; English. | | |
| XX | | | |
| CC | The present sequence represents the human KCNQ5 (also called KCN6q) gene | | |
| CC | which encodes a voltage-gated potassium channel protein. Human KCNQ5 | | |
| CC | has ophthalmological, auditory, central nervous system (CNS), | | |
| CC | cardioactive, anticonvulsant, gastrointestinal and muscular active | | |
| CC | activities. Sequences and methods from the present invention are useful | | |
| CC | for identifying activators or inhibitors of KCNQ5 protein. These | | |
| CC | activators and inhibitors are useful for treating Stargardt-like macular | | |
| CC | dystrophy, cone-rod dystrophy, Salla disease, age-related macular | | |
| CC | degeneration, other forms of macular degeneration, deafness, epilepsy, | | |
| CC | and different forms of neuropsychiatric, heart, gastrointestinal, and | | |
| CC | muscle disorders. Stargardt-like macular dystrophy and cone-rod | | |
| CC | dystrophies are located at chromosome 6q. | | |
| XX | | | |
| XX | Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 72 other; | | |

| Query Match | 36.1% | Score 963.4 | DB 21: | Length 125910: |
|-----------------------|--|---------------------|---------------|----------------|
| Best Local Similarity | 99.9% | Pred. No. 2.8e-272: | | |
| Matches 964: | Conservative | 0: | Mismatches 1: | Indels 0: |
| | | | | Gaps 0 |
| QY 1703 | AGGTACAGTCCATAGAGTCAAGCTGACGTGACCTACTAGACATCTATCAACAGGTCCTTC | 1762 | | |
| Db 123624 | AGGTACAGTCCATAGATTCGAATCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTC | 123683 | | |
| QY 1763 | GGAAGAAGCTCTGGCTTCAGACCTCGCTTTGGCTTCATTTCCAGATTCCTCACCCTTTTGGATGTG | 1822 | | |
| Db 123684 | GGAAGAAGCTCTGGCTTCAGACCTCGCTTTGGCTTCATTTCCAGATTCCTCACCCTTTTGGATGTG | 123743 | | |
| QY 1823 | AACAGACATCTGACATCAAAAGCCCTGTGGATGAGCAAGAATCTTTCGGCTTCGGCACA | 1882 | | |
| Db 123744 | AACAGACATCTGACATCAAAAGCCCTGTGGATGAGCAAGAATCTTTCGGCTTCGGCACA | 123803 | | |
| QY 1883 | ACAGTGGCTGCTTATTCAGATTCACATCTAGTCCACATCTCGAGAGGCTTCGAGTTTCATTC | 1942 | | |
| Db 123804 | ACAGTGGCTGCTTATTCAGATTCACATCTAGTCCACATCTCGAGAGGCTTCGAGTTTCATTC | 123863 | | |
| QY 1943 | TGAGCCCAAAATGAGTTCAGTGGCCGACGCTTCTAGCGGCTTGAAGCCCTACTATGACACATTC | 2002 | | |
| Db 123864 | TGAGCCCAAAATGAGTTCAGTGGCCGACGCTTCTAGCGGCTTGAAGCCCTACTATGACACATTC | 123923 | | |
| QY 2003 | AAGCAACACAGTGGCAATTAAGTCAAGCGATGAGGCTCAGACAGTGGCAGCCACCAACCA | 2062 | | |
| Db 123924 | AAGCAACACAGTGGCAATTAAGTCAAGCGATGAGGCTCAGACAGTGGCAGCCACCAACCA | 123983 | | |
| QY 2063 | TTGCAACCAAAATTAATATAGCGCACCCAGCCAGCAGCAGCCCAACACTTTTACATCTCCAC | 2122 | | |
| Db 123984 | TTGCAACCAAAATTAATATAGCGCACCCAGCCAGCAGCAGCCCAACACTTTTACATCTCCAC | 124043 | | |
| QY 2123 | CTCCCTCCCTCCACCATCAAGCATCTGCGCCAGAGCCAGAAATCTGCAACCTTAACCTGAC | 2182 | | |
| Db 124044 | CTCCCTCCCTCCACCATCAAGCATCTGCGCCAGAGCCAGAAATCTGCAACCTTAACCTGAC | 124103 | | |
| QY 2183 | GCTTACAGAAAGCATTTCTGAGCTACCACTGCTGCTTGGCTCCAAAGAAATGTTTC | 2242 | | |
| Db 124104 | GCTTACAGAAAGCATTTCTGAGCTACCACTGCTGCTTGGCTCCAAAGAAATGTTTC | 124163 | | |
| QY 2243 | AGGTGACACAGTCAAAATCTCACCAAGGACCGTTCTATGAGAAAGACTTTGGACATGGAG | 2302 | | |
| Db 124164 | AGGTGACACAGTCAAAATCTCACCAAGGACCGTTCTATGAGAAAGACTTTGGACATGGAG | 124223 | | |
| QY 2303 | GAGAAACTCTGTTGTCTGCTGTCCCATGGTGCCGAAGCACTTGGGCAAACTTGTCTGTG | 2362 | | |
| Db 124224 | GAGAAACTCTGTTGTCTGCTGTCCCATGGTGCCGAAGCACTTGGGCAAACTTGTCTGTG | 124283 | | |
| QY 2363 | TGCAAAACCTGATCAGGTTCGACCGAGGAACCTGATATATACACTTTTCAAGGAGTGAAGTCAA | 2422 | | |
| Db 124284 | TGCAAAACCTGATCAGGTTCGACCGAGGAACCTGATATATACACTTTTCAAGGAGTGAAGTCAA | 124343 | | |
| QY 2423 | GTGGCTCCGAGAGCGCCCAAGATTTTATACCCCAATGTGAGAGCAATCCAAATTTTATAA | 2482 | | |
| Db 124344 | GTGGCTCCGAGAGCGCCCAAGATTTTATACCCCAATGTGAGAGCAATCCAAATTTTATAA | 124403 | | |
| QY 2483 | CTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTTGGATGCCGACCCGAGC | 2542 | | |
| Db 124404 | CTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTTGGATGCCGACCCGAGC | 124463 | | |
| QY 2543 | CTGCCACGGAACTGGCTTTGATCGACCTCTATAGAGCTGGAAGGTCACGATCATCTC | 2602 | | |
| Db 124464 | CTGCCACGGAACTGGCTTTGATCGACCTCTATAGAGCTGGAAGGTCACGATCATCTC | 124523 | | |
| QY 2603 | AGAGCATTTTGTAAAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCAAACTGA | 2662 | | |
| Db 124524 | AGAGCATTTTGTAAAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCAAACTGA | 124583 | | |
| QY 2663 | AATAA 2667 | | | |
| Db 124584 | AATAA 124588 | | | |

| | | | |
|---|------|---|------|
| D | 1100 | ATGCGGAGGCAACCTCATCCAGGCTGGCTGGCGCTCTACTCCACGATATGAGCGG | 1150 |
| Q | 1057 | GTTTTCATTGCAACCTGGAAGCCACACTTTGAAGGCTTCACAC----- | 1100 |
| D | 1160 | GCTTACCTGACAGCGCACCCTGTACTACTATGACAGATATCTCCATCTTCAGAGACTG | 1219 |
| Q | 1101 | ----- | 1100 |
| D | 1220 | GCCCTCTGTTGAGCAGCTGCACGGGCGCCGATGGGGGCTTACGGCCCTGGAGGTG | 1279 |
| Q | 1101 | ----- | 1100 |
| D | 1280 | CGGGGGGCGCGGTACCGGAGGAGACCCCTCCGTTACCGCCGCTTGGCACCTGGCAC | 1339 |
| Q | 1101 | -----CTGCAGCCCTACCATTCAGACGCTAACTTTAAGAGCGA | 1140 |
| D | 1340 | CGGGCGGCGAGCACCTCTCTTTCCTGGGGAAGGACGCGGTGGGCATCAAAAGACCG | 1399 |
| Q | 1141 | GTGGCCATGGCTAGGCCCCAGGGGGCCAGAGATTT-----AAGAGCGACAAAGCCTCAGTA | 1194 |
| D | 1400 | ATCCGATATGGAGCTCCAGCGGGCGAGCGGGTCTTTCCAAAGCAGCAGCTGGCACCTCCA | 1459 |
| Q | 1195 | GGTGACAGGAGGTCCCAAGCAGCAGCATCAGAGCCGAGG--GCAGTCCCAACAAAGT | 1251 |
| D | 1460 | ACAATGGCCACTCTCCCAAGCAGCGAGGAGCGAGTGGGTGAGGCCACAGCCCAACAGGTG | 1519 |
| Q | 1232 | CAGAAGAGCTGAGCTTCAACACCGACACCCTGTTCCGGCTTCGCTGGCGCTCAAAAGT | 1311 |
| D | 1520 | CAAAAGAGCTGAGGCTTCATAGTACCCGACCCCGCTTCCGGGATCTCTGAAACATC----- | 1573 |
| Q | 1312 | TCTCAGCCAAACCAAGTGTAGATGTGTGACACAGCCCTTGGCACTGTATGTATGAT | 1371 |
| D | 1574 | -----AAACCCCGGACCTCTGCTGAGAGATCCCC---CTCTCAGAGCAAGTATGACAGAG | 1621 |
| Q | 1372 | GAAAAAGATGCGCAGTGTGATGTATCAGTGGAGAGACTCACCACCACTTAAACCTGTC | 1431 |
| D | 1622 | GAGAGAGAGCTACCACTGTGAGCTGCACGGTGGAGCAGATCATGCTCTGTGAAGCAGTC | 1681 |
| Q | 1432 | ATTGAGGCTATCAGATTTATGAATTTCTATGTTGCAAAACGGAAATTAAAGAAACGTTA | 1491 |
| D | 1682 | ATCCGCTCCATAGAGTTCTCAAGTTCTCTGGTGGCCAAAAGAAATTCMAAGAGACACTG | 1741 |
| Q | 1492 | CGTCCATATGATGTAAAGATGTCAATTGAACAATATTTCTGCTGGTCATCTGGACATGTG | 1551 |
| D | 1742 | CGACCGTACGAGGTGAAGAGCGTCAATTGACACGATCTACAGCAGGCCACTCTGGACATGCTG | 1801 |
| Q | 1532 | TGTAGATTTAAAGCCTTTCAACACGCTGTTGATCAAAATTTCTTGGAAAAAGCC---AATTC | 1608 |
| D | 1802 | GGCCGAGTAAAGAGCTGTCAAACTGGGGTGGACCAAAATTTGTGGGTGGGGGCCCGGGGAC | 1861 |
| Q | 1609 | ACATCAGATTAAGAGAGCGGAGAGAAATTAACAGCAACATGACAGACACAGACGATCTC | 1668 |
| D | 1862 | AGGAAGGCCCGGAGAGAGGCGACAAAGGGGCCCTCCGACGCGAGAGTGTGATGAATATC | 1921 |
| Q | 1669 | AGTATGCTCGGTGGGTGCTGCAAGGTTGAAAAAAGGTACAGTCCATATAGATCCAACTG | 1728 |
| D | 1922 | ACCATGATGTGGAGCGCTGTGTCAAGGTGGAGAACAGGTGCAATTCATTCAGACACAAAGCTG | 1981 |
| Q | 1729 | GACTGCTACTAGACATCTATCAACAGGCTCTTTCGGAAGAGGCTGTGGCTCGACCTCGCT | 1788 |
| D | 1982 | GACCTGCTTTGGGCTTCTATTTTGGCGCTGCTGC-----GCTTGGCACCTCGGCCACG | 2033 |
| Q | 1789 | TTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCTATCAAGCCCT | 1846 |
| D | 2036 | CTGGGGCGCGTGCAGATGCGCTGTGTGACCCGACATCACTCTCAGCTACACAGCCCT | 2095 |
| Q | 1849 | GTGATAGCAAAATCTTTTCGGGTTCCGCAAMA | 1882 |
| D | 2096 | GTGGACACGAGGACATCTCCGTTCCGCAAGA | 2129 |

RESULT 12
AAX57140

| | | |
|----|--|--|
| ID | AAK57140 | standard: DNA; 2273 BP. |
| XX | | |
| AC | AAK57140: | |
| XX | | |
| DT | 22-JUL-1999 | (first entry) |
| XX | | |
| DE | Mouse KCNQ2 cDNA. | |
| XX | | |
| KW | KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis; | |
| KW | benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; | |
| KW | JME; rolandic epilepsy; mutant; treatment; screening; epilepsy; | |
| KW | detection; gene therapy; drug screening; ss. | |
| XX | | |
| OS | Mus musculus. | |
| XX | | |
| FT | key | Location/Qualifiers |
| FT | CDS | 1..2273 |
| FT | | /*tag= a |
| FT | | /product= "KCNQ2" |
| FT | | /note= "Partial sequence, no stop codon given" |
| XX | | |
| PN | W09921875-A1. | |
| XX | | |
| PD | 06-MAY-1999. | |
| XX | | |
| PF | 23-OCT-1998; | 98WO-US22375. |
| XX | | |
| PR | 24-OCT-1997; | 97US-0063147. |
| XX | | |
| PA | (UTAH) UNIV UTAH RES FOUND. | |
| XX | | |
| PI | Charlier C, Leppert MF, Singh NA; | |
| XX | | |
| DR | WPI: 1999-312938/26. | |
| DR | P-PSDB: AAY08345. | |
| XX | | |
| XX | Nucleic acid encoding potassium channels KCNQ2 and 3 | |
| PT | | |
| PS | Claim 1; Page 153-156; 195pp; English. | |
| XX | | |
| CC | This invention describes novel human and mouse potassium channel proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for diagnosis and prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves in cell-free form) are used to screen for agents that can be used to treat or prevent these forms of epilepsy. Fragments of the encoding nucleic acids are used as probes or primers, either for detecting mutations or for isolation of related sequences, while the complete sequences may be used in gene therapy to provide wild-type protein. Antibodies specific for mutant or wild-type proteins are used as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are useful in rational design of drugs and therapeutically (in replacement therapies). The forms of epilepsy associated with mutations in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are manifest), and better treatment options will be available. | |
| XX | Sequence 2273 BP; 486 A; 670 C; 653 G; 448 T; 16 other: | |

| | | | | | | | | | | |
|----|-------------|---|--------------|-------|------------|-----------|--------|--------|-------|---|
| | Query Match | Similarity | 18.3% | Score | 489.2; | DB | 20; | Length | 2273; | |
| | Best Local | Similarity | 57.0%; | Pred. | Nm. | 2.7e-133; | | | | |
| | Matches | 1020; | Conservative | 2; | Mismatches | 667; | Indels | 99; | Gaps | 4 |
| Oy | 64 | GGCCTGACTACTCTGGGCAACCGCCGGCAGACGGTGTGGTGCGCGCGCGTGGCCAGAG | 123 | | | | | | | |
| | | | | | | | | | | |
| Db | 67 | GGCTTCGTGGGGCTGGACCCCGGCCGAGCCCAANTCCACACGGACGGCGCMNCTACTATC | 126 | | | | | | | |
| Oy | 124 | GAGACCGCCCGGGGCAAGCAGAGGGGCCCGCATGAGGCTGCTGGGGAAAGCCCTCTTTAC | 183 | | | | | | | |
| | | | | | | | | | | |
| Db | 127 | GGGGGCTCCGAAGCCCCCAAGCGGGCANCNNITTTAGACAAGCCCGCGGAGGGCGGCGCG | 186 | | | | | | | |
| Oy | 184 | ACGAGTAGCCAGAGCTGCCCGCGCAACGTCAAGTACCGGCGGGTGTGAGACTACTCTGTAC | 243 | | | | | | | |

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Db 187 GGANCCGGAGAGCCCCCAANMGCAAGCCTTCACCGCAAGCTGAGATTTCTCTAC 246
QY 244 AACCTGCTGGAGAACCCCGGGCGTTTCATCTACACGCTTTCCTCTT 303
Db 247 AACGTGTAGAGCGGCCCGGCTGCTGCTATCTACACGCTTTCCTCTG 306
QY 304 GTCCTTGTCTGATTTGTGATGTTTCTTCTACATCCCTGAGACACCAAAATTTGGC 363
Db 307 GTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 366
QY 364 TCAAGTTGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 423
Db 367 GAGGGGCGCTCTACATCTTGAATCTGATCTGATCTGATCTGATCTGATCTGAT 426
QY 424 ATTGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 483
Db 427 GTGAGGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 486
QY 484 TTTGCTGAAAAGCCCTCTGTTATAGATACATCTTCTTATGCTTCAATACAGTT 543
Db 487 TTTGCCAGGAAGCCGTTCTGTGTATGATATCATGATGATGATGATGATGATGAT 546
QY 544 GTTTCCTCAAAATCTGAGGTAATATTTTGCACGCTGCTGATCTGATCTGATCTG 603
Db 547 CTGGCTGCTGCTTCCAGGGCAATGCTTTCACCATCTGCGCTTCGAGCTTGGCGTTC 606
QY 604 CTACAGATCTCCGCAATGCTGCTGATGATGATGATGATGATGATGATGATGAT 663
Db 607 TTGCAATATCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
QY 664 TCAAGTGTATGCTCTACAGCAAGAAATTAATCAAGCTTGTATAGATTTTGTGT 723
Db 667 TCGGTAGTCTACGCTACAGCAAGAAATGATGATGATGATGATGATGATGATGAT 726
QY 724 CTATATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 783
Db 727 CTATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 786
QY 784 ACATATGACAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
Db 787 ACCTAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846
QY 844 AAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 903
Db 847 AAGTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
QY 904 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 963
Db 907 TCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 966
QY 964 CAACACCGCCGAGAACTTTGAGAAAAGAAAGAACCCAGCTGCAACCTTATTCAGT 1023
Db 967 CAGCATCTGCGAAAACACTTTGAGAAAAGGAGAACCTCTGGGAGATCTATCCAGCT 1026
QY 1024 GTTGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1047
Db 1027 GCTTGGAGATTTCTATGCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1086
QY 1048 ---GAGAAATCTGTTTTCATTTGCAACCTGGAAGCCACACTTGAAGCCTTCAACCTG 1104
Db 1087 TACGAGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1146
QY 1105 AGCCCTTAC-----AATCAGAAGCTAGATTTA 1132
Db 1147 AGACTCATCTCCACTCTGAAACAGCTGAGCTGCTGAGAAATCTCAAGAGCAAAATCTGGA 1206
QY 1133 AGAGAGGAGTGCAGATGCTGATGCCCAAGGGCCAGAGATTAATAGAGCCGCAAGCCTCAG 1192
Db 1207 CTCACCTTCAGGAAGGAGCCACAGAGCAGATCAACCAAGCCCGAGGAGATGGCTGCC 1266
QY 1193 TAGGTGACGAGAGGTCCCAAGACGACATCACAGC----- 1229

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Db 1267 AAGGGAAGGGGTCTCCCAAGGCCACAGAGCTCCGCGGTCCCACTGGCGATCAGAGT 1326
QY 1230 -CGAGGGAGTCCACCACAAAGTGACAGAGAGCTGGAGCTTCAAGACCAAGCCGCTTC 1287
Db 1327 CTGATGACAGCCCGAGCAAGAGTGTCCCAAGAGCTTGAGCTTTGGTACCCGACGCACCA 1386
QY 1288 CGGCGCTCGCTGGGCCCTCAAAAGTCTCAGCCAAACCAAGATGATGCTGACACAGCC 1347
Db 1387 CGCGAGGCTTTCGATCAAGAGGTGATGATGATGATGATGATGATGATGATGATGAT 1446
QY 1348 CTGCGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
Db 1447 CCGGAGGAGGACATCTGATGAGGACAAACAGAGCTGTAACTGCGAGTTGTGATGATGAT 1506
QY 1408 CTACCCCAACCACTTAACTGATCTGAGCTATCAAGATTAATGAAATTTGATGATGCA 1467
Db 1507 CTTACCCCTGGCTCAAAAGATGATGATGATGATGATGATGATGATGATGATGAT 1566
QY 1468 AAACGGAAGTTTAAAGAAAGTACGTCATGATGATGATGATGATGATGATGATGAT 1527
Db 1567 AAGCGAAAGTTCAAAAGAGAGTCTGCGCCATATGATGATGATGATGATGATGATGAT 1626
QY 1528 TCTGCTGCTCATCTGACATGTTGTGATGATGATGATGATGATGATGATGATGATGAT 1587
Db 1627 TCGGCTGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1686
QY 1588 ATTCTTGGAAAAGGGCAATACATCAGATGATGATGATGATGATGATGATGATGAT 1647
Db 1687 ATTGTGGGCGGGGCCCAACAAATTAACGATTAAGGA--TCGACACAAAGGCCAGGAA 1743
QY 1648 CATGAGACCAACAGCATCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1707
Db 1744 ACGAGACTGCGCGAAGACCCACACATGATGATGATGATGATGATGATGATGATGAT 1803
QY 1708 CAGTCCATGAGTCCAAAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1755
Db 1804 TTGTCATGGAAGAAAGCTGCACTTCTGCTGATGATGATGATGATGATGATGATGAT 1851

RESULT 13
AAK26588
ID AAK26588 standard; DNA; 2169 BP.
XX
XX AAK26588;
XX
XX 16-JUN-1999 (first entry)
XX
XX Nucleotide sequence of murine KCNQ2 (formerly known as (KvLRI)).
XX
XX KCNQ protein; nervous system-specific potassium channel;
XX neuronal excitability; neurotransmitter release; KCNQ modulator;
XX ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
XX age-associated memory loss; learning deficiency; motor neuron disease;
XX epilepsy; stroke; ss.
XX
XX Mus sp.
XX
XX OS
XX
XX FH
XX Key 1.2169
XX CDS /*tag= a
XX
XX PN W09907832-A1.
XX
XX PD 18-FEB-1999.
XX
XX XX 26-JUN-1998; 98WO-US13276.
XX
XX PF 12-AUG-1997; 97US-0055599.
XX
XX PR
XX
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Binar MA, Dworetzky S, Gribkoff VK, Levesque PC;
XX Little WA, Neubauer MG, Yang W;
PI

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OM nucleic - nucleic search, using sw model
Run on:

January 11, 2003, 15:51:17

Search time 2434 Seconds
(without alignments)

17745.835 Million cell updates/sec

Title: US-09-810-796-3
Perfect score: 2667

Sequence: 1 atgaagatgtaggaacgcggg.....ctcagtcacactgaataaa

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched:

16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 32308132
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: qb_estli:*
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23: em_gss_man:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_trod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 637.2 | 23.9 | 658 | 10 | BE158938 |
| 2 | 553.8 | 20.8 | 734 | 12 | BG532543 |
| 3 | 536.4 | 20.1 | 547 | 13 | B1034993 |
| 4 | 530.8 | 19.9 | 570 | 13 | B1033850 |
| 5 | 524.4 | 19.7 | 679 | 10 | BE647997 |
| 6 | 522 | 19.6 | 908 | 12 | BE240146 |

| | | | | | |
|----|-------|------|------|----|----------|
| 7 | 516.8 | 19.4 | 584 | 10 | AM049888 |
| 8 | 487.4 | 18.3 | 506 | 12 | BP95996 |
| 9 | 487 | 18.3 | 632 | 10 | BE624101 |
| 10 | 474 | 17.8 | 491 | 12 | BP959488 |
| 11 | 454.8 | 17.1 | 997 | 10 | BB069854 |
| 12 | 415.8 | 15.6 | 435 | 12 | BE943257 |
| 13 | 414.6 | 15.5 | 469 | 10 | BE103175 |
| 14 | 403 | 15.1 | 517 | 12 | BE954375 |
| 15 | 400.8 | 15.0 | 568 | 14 | B0339931 |
| 16 | 378.4 | 14.2 | 477 | 17 | A2443500 |
| 17 | 354.6 | 12.7 | 528 | 13 | B1290441 |
| 18 | 339.8 | 12.3 | 434 | 12 | BG732557 |
| 19 | 310.8 | 11.7 | 427 | 12 | BF523361 |
| 20 | 302.2 | 11.3 | 914 | 12 | BF312386 |
| 21 | 301.4 | 11.3 | 515 | 12 | BF962769 |
| 22 | 298.8 | 11.2 | 634 | 9 | A1589812 |
| 23 | 279.8 | 10.5 | 597 | 10 | BE260338 |
| 24 | 275.4 | 10.3 | 625 | 10 | BB666833 |
| 25 | 270.2 | 10.1 | 1004 | 14 | BQ219245 |
| 26 | 266.4 | 10.0 | 920 | 12 | BF317072 |
| 27 | 259.8 | 9.7 | 266 | 14 | B0340178 |
| 28 | 256.8 | 9.6 | 541 | 9 | A1968605 |
| 29 | 249.8 | 9.4 | 626 | 10 | BB635544 |
| 30 | 242.4 | 9.1 | 267 | 12 | BF945327 |
| 31 | 241 | 9.0 | 771 | 9 | A151016 |
| 32 | 239.4 | 8.6 | 502 | 9 | A1418222 |
| 33 | 230 | 8.6 | 766 | 11 | AK020325 |
| 34 | 227.6 | 8.5 | 282 | 9 | A1603318 |
| 35 | 217.8 | 8.2 | 469 | 9 | A1864554 |
| 36 | 217.8 | 8.2 | 655 | 12 | BF432555 |
| 37 | 216 | 8.1 | 300 | 9 | A1576388 |
| 38 | 214.8 | 8.1 | 438 | 14 | B0285922 |
| 39 | 207.4 | 7.8 | 224 | 12 | BP954374 |
| 40 | 206.4 | 7.7 | 698 | 13 | BM640404 |
| 41 | 205.6 | 7.7 | 407 | 9 | A1871198 |
| 42 | 202 | 7.6 | 448 | 10 | AV838434 |
| 43 | 199.2 | 7.5 | 622 | 10 | BE257127 |
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ALIGNMENTS

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LOCUS BE158938
DEFINITION MRO-HT0404-210200-001-c04 HT0404 Homo sapiens CDNA, mRNA sequence.
ACCESSION BE158938
VERSION BE158938.1 GI:8621659
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 658)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Ludwig Institute for Cancer Research
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Brazil

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JOURNAL MEDLINE
COMMENT

Email: asimpson@judwig.org, br
This sequence was derived from the FAPESP/LICR Human Genome
Project. This entry can be seen in the following URL
(http://www.judwig.org.br/scripts/gethtml2.pl?cl=6t2-MR0-HT0404-210
200-001-c046t3=2000-02-21&t=1)
Seq primer: puc 18 forward
High quality sequence stop: 657.
Location/Qualifiers

FEATURES

1. 658
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0404"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site:1: Small;
Site:2: Small; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research) of
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
Location/Qualifiers

BASE COUNT 181 a 175 c 153 g 149 t

Query Match 23.98; Score 637.2; DB 10; Length 658;
Best Local Similarity 99.58; Pred. No. 7e-146; 3; Indels 0; Gaps 0;
Matches 639; Conservative 0; Mismatches

831 TGGCTATGAGCAAAACCCCTACTGCTGGGAGGAGTTGCTTCTGAGGCTTTGC 890
17 TGGCTATGAGCAAAACCCCTACTGCTGGGAGGAGTTGCTTCTGAGGCTTTGC 76
891 ACTCTTGGCATTTCTTTCTTGGCACTTCTGCGGATTTCTTCTGAGGCTTTGC 136
77 ACTCTTGGCATTTCTTTCTTGGCACTTCTGCGGATTTCTTCTGAGGCTTTGC 1010
951 AAAAGTCAAGAACACACCGCCAGAACACTTGAAGAAAGAACCCAGCTCCCA 196
137 AAAAGTCAAGAACACACCGCCAGAACACTTGAAGAAAGAACCCAGCTCCCA 1070
1011 CCTCATTCAGTGTGTTGGCGTGTAGTACGAGCTGATGAGAAATCTGTTCCATTGCAAC 256
197 CCTCATTCAGTGTGTTGGCGTGTAGTACGAGCTGATGAGAAATCTGTTCCATTGCAAC 1130
1071 CTGGAAGCCCACTTTGAAGGCTTGCACACCTGCAGCCCTACCAATCGAAGCTAAGTTT 316
257 CTGGAAGCCCACTTTGAAGGCTTGCACACCTGCAGCCCTACCAATCGAAGCTAAGTTT 1190
1131 TAAAGAGCGAGTGCAGTGGCTAGCCCAAGGGGCCAGAGTATTAAAGCCGACAGCTTC 376
317 TAAAGAGCGAGTGCAGTGGCTAGCCCAAGGGGCCAGAGTATTAAAGCCGACAGCTTC 1250
1191 AGTAGGTGACAGAGGTGCCCAAGACACGACATCAGACGCGGAGGAGTCCACCAAGT 436
377 AGTAGGTGACAGAGGTGCCCAAGACACGACATCAGACGCGGAGGAGTCCACCAAGT 1310
1251 GCAGAGAGCTGGAGCTTCAACGACGACGACGACGACGACGACGACGACGACGACGAC 496
437 GCAGAGAGCTGGAGCTTCAACGACGACGACGACGACGACGACGACGACGACGACGAC 1370
1311 TTCTGAGCCAAACAGTATGATGCTGACAGAGCTTGGCACTGATGATGATGATGATGATG 556
497 TTCTGAGCCAAACAGTATGATGCTGACAGAGCTTGGCACTGATGATGATGATGATGATG 1430
1371 TGAAGAAAGATGCTGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 616
557 TGAAGAAAGATGCTGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1472
1431 CATTCGAGCTATCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 658
617 CATTCGAGCTATCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT

RESULT 2

RG532543 734 bp mRNA linear EST 03-APR-2001
LOCUS 602562103F1 NIH_MGC_61 Homo sapiens cDNA IMAGE:4699776 5',
DEFINITION mRNA sequence.
RG532543
ACCESSION RG532543.1 GI:13524082
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 734)
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.femail.nih.gov
Tissue Procurement: ATCC
DNA Library Preparation: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LICK1532 row: F column: 01
High quality sequence stop: 699.
Location/Qualifiers

FEATURES

1. 734
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pMDR-LIB (Clontech); Site:1:
Site:2: Still (99catatggcc);
Still (99ccgctcgcc); Site:3: Still (99ccatattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
adaptor sequence: 5'-ATCTAGAGCGCCGAGCGCGGACGACG-3' and 3' adaptor
sequence: 5'-CACGGCCATATGAGG-3' (30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
Library."
Location/Qualifiers

BASE COUNT 213 a 177 c 165 g 179 t

Query Match 20.88; Score 553.8; DB 12; Length 734;
Best Local Similarity 99.68; Pred. No. 2.5e-125; 2; Indels 0; Gaps 0;
Matches 555; Conservative

2111 TACAGATCCACCTCTCTCCAGGCAATCAGCATGCGCCAGCAAACTCTGGCAC 60
1 TACAGATCCACCTCTCTCCAGGCAATCAGCATGCGCCAGCAAACTCTGGCAC 2230
2171 CTAACTCTGAGGCTTACAGAAAGCATTTCTGACGTCACACCTCTGTTGGCTCCA 120
61 CTAACTCTGAGGCTTACAGAAAGCATTTCTGACGTCACACCTCTGTTGGCTCCA 2290
2231 AGCAAAATGTTGAGTGTGACAGTCAATCTCACCAAGACCGTTCTATGAGAAAGCT 180
121 AGCAAAATGTTGAGTGTGACAGTCAATCTCACCAAGACCGTTCTATGAGAAAGCT 2350
2291 TTGACATGGAGAGAAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
181 TTGACATGGAGAGAAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2410
2351 AATCTTTGCTGTGCAAAACCTGATCAGTGCAGCGAGAACTGAATATACAACTTTCAG 300
241 AATCTTTGCTGTGCAAAACCTGATCAGTGCAGCGAGAACTGAATATACAACTTTCAG

QY 2411 GGAGTGAAGTCAAGTGGCTCCAGAGCCAGCCAGATTTTACCCTCAATGAGGAAATCCCA 2470
 |||||||
 Db 301 GGAGTGAAGTCAAGTGGCTCCAGAGCCAGCCAGATTTTACCCTCAATGAGGAAATCCCA 360
 |||||||
 QY 2471 AATTGTTATATACGATGAAGAGTGGGGTCCCGAAGAGACAGACAGACACTTTTGATG 2530
 |||||||
 Db 361 AATTGTTATATACGATGAAGAGTGGGGTCCCGAAGAGACAGACAGACACTTTTGATG 420
 |||||||
 QY 2531 CCGACCGCAGCCCTGCCAGGGAAGCTGCTTTGCATCAGACTCTCTAAAGACTGGAAGGT 2590
 |||||||
 Db 421 CCGACCGCAGCCCTGCCAGGGAAGCTGCTTTGCATCAGACTCTCTAAAGACTGGAAGGT 480
 |||||||
 QY 2591 CACGATCATCTCAGAGCACTTTTGAAGCAGAGAAAGTACAGATGCCCTCAGCTTGCTTC 2650
 |||||||
 Db 481 CACGATCATCTCAGAGCACTTTTGAAGCAGAGAAAGTACAGATGCCCTCAGCTTGCTTC 540
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 QY 2651 ATGTCAACCTGAATTA 2667
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 Db 541 ATGTCAACCTGAATTA 557
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RESULT 3
 LOCUS BI034993 547 bp mRNA linear EST 14-JUN-2001
 DEFINITION OY2-NN2004-120401-621-g02 NN2004 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BI034993
 VERSION BI034993.1 GI:14441619
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 547)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT

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 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1-QV2&l2-QV2-NN2004-
 120401-621-g02&l3-2001-04-12&l4-1)
 Seq primer: puc 18 forward
 High quality sequence stop: 543.

FEATURES
 source
 Location/Qualifiers
 1..547
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone.lib="NN2004"
 /dev_stage="Adult"

/note="Organ: nervous; normal; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 175 a 127 c 116 g 129 t
 ORIGIN

Query Match 20.1% Score 536.4; DB 13; Length 547;
 Best Local Similarity 98.9%; Pred. No. 4.5e-121;
 Matches 540; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1268 TCAACGACCGAACCCGCTTCCGGCCCTCGTCGCGCTCAAAAAGTTCTCAGCCAAAACAG 1327
 |||||||
 Db 1 TCAACGACCGAACCCGCTTCCGGCCCTCGTCGCGCTCAAAAAGTTCTCAGCCAAAACAG 60
 |||||||

QY 1328 TGATATGATGCTGACACAGCCCTTGGACACTGATGATGATATGATGATGATGATGAT 1387
 |||||||
 Db 61 TGATATGATGCTGACACAGCCCTTGGACACTGATGATGATGATGATGATGATGATGATGAT 120
 |||||||

QY 1388 GTGATGTATGCTGACGAGACCTCCACCCACACTTAACACGTCATTTGGAGTATACAGAA 1447
 |||||||
 Db 121 GTGATGTATGCTGACGAGACCTCCACCCACACTTAACACGTCATTTGGAGTATACAGAA 180
 |||||||

QY 1448 TTATGAATTTTCATGTTGCAAAAGGAAAGTTAAGAAACGTTACGTCATATGATGTA 1507
 |||||||
 Db 181 TTATGAATTTTCATGTTGCAAAAGGAAAGTTAAGAAACGTTACGTCATATGATGTA 240
 |||||||

QY 1508 AAGATGTCATTTGAACAATATTTCTGCTGTCATCTGACATGTTGTGAAATTAAGACC 1567
 |||||||
 Db 241 AAGATGTCATTTGAACAATATTTCTGCTGTCATCTGACATGTTGTGAAATTAAGACC 300
 |||||||

QY 1568 TTCAACACGCTGTTGATCAAAATTTCTTGAAAGGCAAAATGACATCAATTAAGAGACC 1627
 |||||||
 Db 301 TTCAACACGCTGTTGATCAAAATTTCTTGAAAGGCAAAATGACATCAATTAAGAGACC 360
 |||||||

QY 1628 GAGAGAAATTAACAGCAACATGAGACACAGACGATCTGATGATGCTGCTGCGGTGG 1687
 |||||||
 Db 361 GAGAGAAATTAACAGCAACATGAGACACAGACGATCTGATGATGCTGCTGCGGTGG 420
 |||||||

QY 1688 TCAAGGTTGAAAAACAGTTCAGTCCATGATGATGATGATGATGATGATGATGATGAT 1747
 |||||||
 Db 421 TCAAGGTTGAAAAACAGTTCAGTCCATGATGATGATGATGATGATGATGATGATGATGAT 480
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QY 1748 ATCAACAGTCTCTCGGAAAGGCTCTCCAGCCCTCGCTTGGCTTCATTTGAGATCC 1807
 |||||||
 Db 481 ATCAACAGTCTCTCGGAAAGGCTCTCCAGCCCTCGCTTGGCTTCATTTGAGATCC 540
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QY 1808 CACCTT 1813
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 Db 541 CACCTT 546
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RESULT 4
 LOCUS BI033850 570 bp mRNA linear EST 14-JUN-2001
 DEFINITION OY2-NN2003-080301-615-c09 NN2003 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BI033850
 VERSION BI033850.1 GI:14440476
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 570)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT

CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922

Fax: +55-11-2707001
 Email: asimposon@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Genome
 Project. This entry can be seen in the following URL:
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV2&cl2=QV2-NN2003-
 080301-615-c09&cl3=2001-03-08&cl4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 570.

FEATURES

Location/Qualifiers
 1..570

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="NN2003"

/dev_stage="Adult"

/note="Organ: nervous normal; Vector: puc18; Site:1: Sma1;
 Site:2: Sma1: A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 135 a 122 c 131 g 182 t

ORIGIN

Query Match 19.9%; Score 530.8; DB 13; Length 570;
 Best Local Similarity 98.7%; Pred. No. 1.1e-119;
 Matches 535; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1303 CTCGAAGTCTCCAGCAAAACAGATAGATGTCGACACAGCCCTTGACATGATGAT 1362

DB 542 CTTCAAATTCCTCAGCAAAACAGATAGATGTCGACACAGCCCTTGACATGATGAT 483

OY 1363 GTATATGATGAAAAAGATCCAGTGTGATGATCAAGTGAAGACCTCACCACCACTT 1422

DB 482 GTATATGATGAAAAAGATCCAGTGTGATGATCAAGTGAAGACCTCACCACCACTT 423

OY 1423 AAAAGTGTCTCGAGCTCTCAGATTTAATGAAATTCATGTTGCAAAAGGAGTTAAG 1482

DB 422 AAAAGTGTCTCGAGCTCTCAGATTTAATGAAATTCATGTTGCAAAAGGAGTTAAG 363

OY 1483 GAAAGTGTCTCGAGCTCTCAGATTTAATGAAATTCATGTTGCAAAAGGAGTTAAG 1542

DB 362 GAAAGTGTCTCGAGCTCTCAGATTTAATGAAATTCATGTTGCAAAAGGAGTTAAG 303

OY 1543 GACATGTTGTGATAGATTTAAAGCCCTTCAACACGCTGTTATCAATTCCTTGGAAAAAGG 1602

DB 302 GACATGTTGTGATAGATTTAAAGCCCTTCAACACGCTGTTATCAATTCCTTGGAAAAAGG 243

OY 1603 CAATTCACATCAGATTAAGAAAGCCGAGCAAAATACACAGAACATGAGACCAAGAC 1662

DB 242 CAATTCACATCAGATTAAGAAAGCCGAGCAAAATACACAGAACATGAGACCAAGAC 183

OY 1663 GATTCAGTATGCTCGTGGGTGTCAGGTTGAAAAACAGGTACAGTCCATAGAGTCC 1722

DB 182 GATTCAGTATGCTCGTGGGTGTCAGGTTGAAAAACAGGTACAGTCCATAGAGTCC 123

OY 1723 AAGCTGAGATGCTCTACTAGACATCTATCAACAGGTCTTGGAAAAAGGCTCGCTCAGCC 1782

DB 122 AAGCTGAGATGCTCTACTAGACATCTATCAACAGGTCTTGGAAAAAGGCTCGCTCAGCC 63

OY 1783 CTCGCTTGGCTCATTCCTCGATGCCACCTTTTGAATGTGAAGACATCGATATCAAA 1842

DB 62 CTCGCTTGGCTCATTCCTCGATGCCACCTTTTGAATGTGAAGACATCGATATCAAA 3

OY 1843 AG 1844

DB 2 AG 1

RESULT 5 679 bp mRNA linear EST 06-SEP-2000
 BE647997/c
 LOCUS BE647997
 DEFINITION UI-M-BH1-amr-g-09-0-UI.r1 NIH_BMAP_M_S2 Mus musculus cDNA clone

ACCESSION

UI-M-BH1-amr-g-09-0-UI 5', mRNA sequence.
 BE647997
 BE647997.1 GI:9973817
 EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus.
 ORGANISM Mus musculus.

REFERENCE

1 (bases 1 to 679)
 Bonaldi,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)

AUTHORS

CONTACT: Chin, H

JOURNAL

97044477

MEDLINE

97044477

COMMENT

Contact: Chin, H

National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890

Email: mst@mail.nih.gov

cDNA library preparation: M.B. Soares lab Clone distribution:
 Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
 should be noted that Bento Soares is generating a small number of
 additional specialized non-redundant arrays of BMAP cDNAs whose
 availability will be considered under appropriate and limited
 collaborative arrangements

Seq primer: M13 Reverse.

Location/Qualifiers

1..679

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone_id="UI-M-BH1-amr-g-09-0-UI"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pTR3D-Pac (Pharmacia) with a modified
 polylinker. Site:1: Not I; Site:2: Eco RI; The
 NIH_BMAP_M_S2 library is a subtracted library derived from
 NIH_BMAP_M_S1, which in turn is a subtracted library from ten
 derived from a mixture of normalized libraries from ten
 regions of the mouse brain (cerebellum, brain stems,
 olfactory bulbs, hypothalamus, cortex, amygdala, basal
 ganglia, pineal gland, striatum, hippocampus). The driver
 used for subtraction consisted of a pool of 5,000 clones
 from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
 obtained from non-normalized and normalized mouse brain
 spinal cord libraries."

BASE COUNT 152 a 150 c 172 g 205 t

ORIGIN

Query Match 19.7%; Score 524.4; DB 10; Length 679;
 Best Local Similarity 88.9%; Pred. No. 4.2e-118;
 Matches 567; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

OY 1402 GAAGACCTCAGCCCAACCACTTAAACTGTCATCGATCAGAAATTAATGAAATTTCAAT 1461

DB 639 GAAGACCTCAGCCCAACCACTTAAACTGTCATCGATCAGAAATTAATGAAATTTCAAT 580

OY 1462 GTTGCAAAACGGAAGTTTAAGAAAGCTTAAGTCAATGATGATTAAGATGTCATTGAA 1521

DB 579 GTTGCAAAACGGAAGTTTAAGAAAGCTTAAGTCAATGATGATTAAGATGTCATTGAA 520

OY 1522 CAATATTCGCTGCTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1581

DB 519 CAATATTCGCTGCTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 460

OY 1582 GATCAAAATCTTGGAAGAGGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1641

DB 459 GATCAAAATCTTGGAAGAGGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 400

OY 1642 GCAGAACATGAGACCAAGACGATCTCAGTATCTCGTGGGTGCTCAAGTTGAAAAA 1701

| Db | 399 | GCAGAACACGAGCAACACAGATGACCCAGCATGCTGCGCGGGTTGTGAAGTTTGAGACAA | 340 | | |
|------------|----------|---|--------------|------|-------------------------|
| QY | 1702 | CAGGTACAGTCATFAGAGTGCAGAGCTGAGACTGCTACTAGACATCTATCAACAGTCTT | 1761 | | |
| Db | 339 | CAGGTCCAGTCCATCGAATCCAGAGCTGAGCTGCTGCTGATATCTATCAACAGTCTTC | 280 | | |
| QY | 1762 | CGGAAAGGCTCTGCTCTCAGCCGCTTGTTGGCTTCATTCAGATCCACACTTTTGAATGT | 1821 | | |
| Db | 279 | CGGAAAGGCTCTGCTCTCAGCCGCTTACTTTGGCATCTCTTCAGATCCCGCTTTTGAATGT | 220 | | |
| QY | 1822 | GAAACAGCATCTGCATCTCAAAAGCCCTGTGGATAGCAAGAATCTTTCGGTTCGGACAA | 1881 | | |
| Db | 219 | GAAACAGCATCTGCATCTCAAAAGCTCTGTGGATAGCAAGAATCTCTGCTCAGACAA | 160 | | |
| QY | 1882 | AACAGTGGCTGCTTATTCAGATCAACTAGTGTCCAAACATCTGAGAGGCTCAGTTCAT | 1941 | | |
| Db | 159 | AACAGGCGCTGCTTTAAAGAGGTGACGAGTCCAAACATCTTAAAGGCTCAGTTCAT | 100 | | |
| QY | 1942 | CTGAGCGCAATGATGATTCAGTCCAGCCAGCATCTTTCACGGCTTAAAGCTTACTATGACAGT | 2001 | | |
| Db | 99 | CTAACACCAATGATGATTCAGTCCAGCATCTTTCATAGCGCTTAAAGCTTACTATGACAGC | 40 | | |
| QY | 2002 | CAAGCAACACAGGTGCCAATTAGTCAAAAGCATGCTC | 2039 | | |
| Db | 39 | CAAGTACCCAGGTACCATGATCAAAATGACGCTC | 2 | | |
| RESULT | 6 | BP240146 | 908 bp | EST | 14-NOV-2000 |
| LOCUS | BP240146 | 601905649P1 NIH_MGC_54 | Homo sapiens | CDNA | clone IMAGE:4133293 5', |
| DEFINITION | | BP240146 | | | |
| ACCESSION | | BP240146 | | | |
| VERSION | | BP240146.1 | GI:11154069 | | |
| KEYWORDS | | EST. | | | |
| SOURCE | | human. | | | |
| ORGANISM | | Homo sapiens | | | |
| REFERENCE | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| AUTHORS | | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| TITLE | | 1 (bases 1 to 908) | | | |
| JOURNAL | | NIH-MGC http://mgc.nci.nih.gov/ . | | | |
| COMMENT | | National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1995) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L16M1034 row: b column: 14 High quality sequence stop: 615. | | | |
| FEATURES | | Location/Qualifiers | | | |
| Source | | 1. 908 | | | |
| | | /organism="Homo sapiens" | | | |
| | | /db_xref="taxon:9606" | | | |
| | | /clone="IMAGE:4133293" | | | |
| | | /clone_lib="NIH-MGC_54" | | | |
| | | /tissue_type="From chronic myelogenous leukemia" | | | |
| | | /lab_host="DH10B (T1 phage-resistant)" | | | |
| | | /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site:1: SfiI (ggcgccctcgcc); Site:2: SfiI (ggccatattgccc); Double-stranded cDNA was prepared from cell line RNA, 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' sequence: 5'-ATTCTAGAGCGCCAGCGCCGCGACATCG-dT(30)BN-3' (where B = A, C, G, or T and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech | | | |

[illegible]

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N. and Hayashizaki, Y.
'M., Kono, H., Okazaki, Y., Muramatsu, M., Sugahara, Y., Shibata, K., Itoh
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
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Hayashizaki, Y.

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10 (11), 1757-1771 (2000)
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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Ishii, Y. and Hayashizaki, Y.
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Funct. Genomics 2 pre, L72-L86 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES

source

Location/Qualifiers
1. 997
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_id="1200002822"
/clone_lib="RIKEN full-length enriched, adult male lung"
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/tissue_type="lung"
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/lab_host="SOLAR"
/note="Site 1: XhoI; Site 2: SstI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGCGCGCCGACCTGAGTATTTTATTAATTAACCCGCCCC 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGAGATCCAGAGCTCAATTAATTAATTAACCCGCCCC 3'],
cDNA was cleaved with XhoI and SstI."

BASE COUNT 172 a 285 c 290 g 248 t 2 others

ORIGIN

Query Match 17.1%, Score 454.8; DB 10; Length 997;
Best Local Similarity 72.9%; Pred. No. 6,4e-101;
Matches 585; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

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277 ATCTACCAAGCTTGTCTCTCTGCTTGTCTGCTTGTCTGCTTGTCTGCTTGTCT 336
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Db 99 GCTTACAGAGCTTGTCTCTCTGCTTGTCTGCTTGTCTGCTTGTCTGCTTGTCT 158
337 ACCATCCCTGAGACACAAATTTGGCTTCAAGTTCCTGTGCTTGTGAGTTCGAGTC 396
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Db 159 ACCATCCAGAGACACACAGAGACTTGGCAACGAGTCTCTTATCTTGAATTCGTGATG 218
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Qy 457 TATAGAGATGGCAAGACACAGAGTTGCTCGAAACCCCTCTGTTATAGATACC 516
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Qy 517 ATTGCTTATTCGCTTCAATAGCAGTTGTTCTGCAAAAACCTAGGATATATTTTGGC 576
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Db 459 CGCGGTGGACACCTGGAAGCTGTTGGGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 518
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Qy 757 GAAAGAGATGCAATTAAGATTTTCTACATATGACAGATGCTGCTGCTGCTGCTGCTGCTGCT 816
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RESULT 12

BP943257/c 435 bp mRNA linear EST 22-JAN-2001
LOCUS BP943257
DEFINITION QV2-NN0045-041000-403-h12 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BP943257
VERSION BP943257.1 GI:12360532
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 435)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Mammalia, Eutheria; Primates; Catarrhini; Homidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Mammalia, Eutheria; Primates; Catarrhini; Homidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

COMMENT
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
 Tel.: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV2&tl-QV2-N00045>)
 041000-403-112&tf3-2000-10-04&ta=1)
 Seq primer: puc 18 forward
 High quality sequence start: 15
 High quality sequence stop: 433.

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| BASE COUNT | 110 a | 94 c | 89 g | 142 t |
| ORIGIN | . | | | |

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| 1720 | 193CATTGAGCATACAGAAATATGAAATTCATGTTGGCAAAACGGAATTTTAAAGAAC | 1487 |
| 1721 | 435 TGTCAATTCGAGCTATCAGAAATATGAAATTCATGTTGGCAAAACGGAATTTTAAAGAAC | 376 |
| 1722 | 1488 GTTACGTCGCAATATGATGATTAAGATATGTCAATTGACAAATATTCCTGCTGTCATCTGGACAT | 1547 |
| 1723 | 375 ATTACGTCGCAATATGATGATTAAGATATGTCAATTAAGCAATATTCCTGCTGTCATCTGGACAT | 316 |
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| BEI03175 | |
| LOCUS | BEI03175 |
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| ACCESSION | U1-R-BT1-agx-h-11-0-U1.s1 U1-R-BT1 Rattus norvegicus cDNA clone |
| VERSION | BEI03175 |
| KEYWORDS | BEI03175.1 GI:8495314 EST. |
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| ORGANISM | Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |

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| REFERENCE | 1 (bases 1 to 469) |
| AUTHORS | Bonaldo,M.F., Lennon,G. and Soares,M.B. |
| TITLE | Normalization and subtraction: two approaches to facilitate gene discovery |
| JOURNAL | Genome Res. 6 (9), 791-806 (1996) |
| MEDLINE | 97044477 |
| COMMENT | Contact: Soares, MB |

| FEATURES | Location/Qualifiers |
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| QY | 107 | GCGGCGTGCGCCTGAGGGAGAGCCCGCGGGCAAGACAGAGGGCGCCGGATGAGCGCTGGG | 167 |
| Dp | 61 | GCGGCGGCGGCTTGAGAGAGAGCCGCGGGCAAGCAGAGGGGCCCGGATGAGCCTTGCG | 122 |
| QY | 167 | GGAGCGCCTCTCTTACACGAGTACCCAGAGCTCCGCGCGCACGTCAAGTACCGCGCG | 222 |
| Dp | 121 | GGAGCGCCTCTCTTACACGAGCAGCAGCAGCAGAGCTGTGGCGCACAGTCAGTACGGAGGG | 180 |
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| QY | 287 | CTTTCGTTTCTCTCTCTGCTCTTGGTGTGCTGATTTTGTACAGTATTCTACCAATCCCTG | 346 |
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ACCESSION BP954375
VERSION BP954375.1 GI:12371650
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 517)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagel,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
COMMENT 20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&tl2=QV2-NN0045-
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High quality sequence stop: 517.
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Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 169 a 106 c 123 g 119 t
ORIGIN
Query Match 15.1%; Score 403; DB 12; length 517;
Best Local Similarity 92.6%; Pred. No. 3.1e-88;
Matches 479; Conservative 0; Mismatches 30; Indels 8; Gaps 5;

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LOCUS QV2-NN0045-081200-535-f03 NN0045 Homo sapiens cDNA, mRNA sequence.
DEFINITION BO339931
ACCESSION BO339931
VERSION BO339931.1 GI:21000109
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 568)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagel,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
COMMENT 20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&tl2=QV2-NN0045-
081200-535-f03&tl3=2000-12-08&tl4=1)
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Location/Qualifiers
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/note="Organ: nervous normal; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)

Profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 176 a 121 c 128 g 143 t

Query Match

15.0%; Score 400.8; DB 14; Length 568;

Best Local Similarity 86.2%; Pred. No. 1.1e-87;

Matches 481; Conservative 0; Mismatches 67; Indels 10; Gaps 3;

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Db 71 ATGACGATATATAGATGTTGGAGAGCCCTTCCGAGACTGATGATATATATGAACAG 130
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Db 431 TGCTGGTGGGGTGCAGAGTTGAAAACAGGTACAGTCCATAGAGTCCAGCTGGACT 490
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QY 1733 GCGTACTAGACATCTATCAACAGGCTCTCGAAAGGCTGTGCTCGCCCTGCTTGG 1792
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 15:52:07 : Search time 74 Seconds

(without alignments)
11052.796 Million cell updates/sec

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Listing first 45 summaries

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6: /cgn2_6/ptodata/1/lna/Dackfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 489.2 | 18.3 | 2273 | 4 | US-09-177-650-88 |
| 2 | 475.6 | 17.8 | 2169 | 4 | US-09-105-058C-22 |
| 3 | 465.4 | 17.5 | 896 | 4 | US-09-105-058C-1 |
| 4 | 427.2 | 16.0 | 2565 | 4 | US-09-105-058C-26 |
| 5 | 427.2 | 16.0 | 2914 | 4 | US-09-177-650-6 |
| 6 | 426.8 | 16.0 | 2814 | 4 | US-09-177-650-90 |
| 7 | 425 | 15.9 | 3287 | 4 | US-09-105-058C-19 |
| 8 | 423.4 | 15.9 | 3232 | 4 | US-09-177-650-1 |
| 9 | 423.4 | 15.9 | 3237 | 4 | US-09-105-058C-95 |
| 10 | 421.4 | 15.8 | 900 | 4 | US-09-105-058C-5 |
| 11 | 420.6 | 15.8 | 900 | 4 | US-09-105-058C-17 |
| 12 | 363.8 | 13.6 | 930 | 4 | US-09-105-058C-7 |
| 13 | 334.2 | 12.5 | 735 | 4 | US-09-105-058C-1 |
| 14 | 267.8 | 10.0 | 2028 | 3 | US-09-135-020-1 |
| 15 | 267.8 | 10.0 | 3181 | 3 | US-09-135-020-1 |
| 16 | 267.8 | 10.0 | 3181 | 4 | US-09-135-020-1 |
| 17 | 267.8 | 10.0 | 3181 | 4 | US-09-135-020-1 |
| 18 | 267.8 | 10.0 | 3181 | 4 | US-09-135-020-1 |
| 19 | 267.8 | 10.0 | 3181 | 4 | US-09-135-020-1 |
| 20 | 267.8 | 10.0 | 3181 | 4 | US-09-135-020-1 |
| 21 | 267.8 | 10.0 | 3181 | 4 | US-09-135-020-1 |
| 22 | 266.6 | 10.0 | 2734 | 3 | US-09-135-021-79 |
| 23 | 266.6 | 10.0 | 2821 | 4 | US-09-135-021-79 |
| 24 | 266.6 | 10.0 | 2821 | 4 | US-09-135-021-79 |
| 25 | 266.6 | 10.0 | 2821 | 4 | US-09-135-021-79 |
| 26 | 258.4 | 9.7 | 2821 | 4 | US-09-135-021-79 |
| 27 | 95.8 | 3.6 | 171 | 4 | US-09-177-650-102 |

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| 28 | 84.8 | 3.2 | 649 | 4 | US-09-177-650-118 | Sequence 118, App |
| 29 | 68.8 | 2.6 | 1021 | 4 | US-09-177-650-127 | Sequence 127, App |
| 30 | 68.2 | 2.6 | 1083 | 4 | US-09-177-650-121 | Sequence 121, App |
| 31 | 67 | 2.5 | 204 | 4 | US-09-177-650-101 | Sequence 101, App |
| 32 | 63.4 | 2.4 | 211 | 4 | US-09-177-650-110 | Sequence 110, App |
| 33 | 63.4 | 2.4 | 245 | 4 | US-09-177-650-115 | Sequence 115, App |
| 34 | 60.8 | 2.3 | 859 | 4 | US-09-177-650-117 | Sequence 117, App |
| 35 | 58.6 | 2.2 | 1292 | 4 | US-09-221-017B-207 | Sequence 207, App |
| 36 | 56.2 | 2.1 | 1117 | 4 | US-09-177-650-120 | Sequence 120, App |
| 37 | 55.2 | 2.1 | 318 | 4 | US-09-177-650-108 | Sequence 108, App |
| 38 | 53.6 | 2.0 | 215 | 4 | US-09-177-650-103 | Sequence 103, App |
| 39 | 52.8 | 2.0 | 238 | 4 | US-09-177-650-105 | Sequence 105, App |
| 40 | 52.4 | 2.0 | 241 | 4 | US-09-177-650-104 | Sequence 104, App |
| 41 | 45 | 1.7 | 7218 | 1 | US-08-232-463-14 | Sequence 14, App |
| 42 | 43.2 | 1.6 | 7218 | 1 | US-08-232-463-14 | Sequence 14, App |
| 43 | 42.8 | 1.6 | 226 | 4 | US-09-105-058C-9 | Sequence 9, App |
| 44 | 42 | 1.6 | 508 | 1 | US-08-318-193-69 | Sequence 69, App |
| 45 | 41.8 | 1.6 | 3424 | 4 | US-09-336-643A-9 | Sequence 9, App |

ALIGNMENTS

RESULT 1
US-09-177-650-88
Sequence 88, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
TITLE OF INVENTION: Charlier, Carole
TITLE OF INVENTION: MUTATED AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 88
LENGTH: 2273
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2271)
US-09-177-650-88

| | | | | |
|-----------------------|--|--------------------|----------------|-------------|
| Query Match | 18.3% | Score 489.2 | DB 4 | Length 2273 |
| Best Local Similarity | 57.0% | Pred. No. 5,7e-136 | | |
| Matches 1020 | Conservative | 2 | Mismatches 667 | Indels 99 |
| 4 | | | | |
| 64 | GGCTGCTACTGCTGGGACCCGCGGCGGCTGCTGGGCGGCGGCGGCTGCTGAGG | 123 | | |
| DB | GGCTGCTGCGGCTGGGACCCGCGGCGGCGGCGGCGGCGGCGGCGGCTGCTGAGG | 123 | | |
| 124 | GAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGCTGAGG | 126 | | |
| DB | GAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGCTGAGG | 126 | | |
| 127 | GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG | 183 | | |
| DB | GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG | 183 | | |
| 184 | ACAGAGACCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG | 186 | | |
| DB | ACAGAGACCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG | 186 | | |
| 187 | GGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG | 243 | | |
| DB | GGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG | 243 | | |
| 244 | AAGCTGCTGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG | 246 | | |
| DB | AAGCTGCTGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG | 246 | | |
| 247 | AAGCTGCTGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG | 303 | | |
| DB | AAGCTGCTGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG | 303 | | |
| 304 | GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 306 | | |
| DB | GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 306 | | |
| 307 | GTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 363 | | |
| DB | GTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 363 | | |

| | | | |
|----|------|---|------|
| QY | 1348 | CTTGACACTGATGTATGTATGATGAATAAAGAGATGCCAGTGTGATGTATCAAGTGGAGAAGC | 1407 |
| Dd | 1447 | CCTGGGAGAGACATCGTTAGAGACAACAAGAGCTGTAACTGGAGTTGTGTGACTAAGAT | 1506 |
| QY | 1408 | CTCACCCACACCATTAAAACTGTCAATTGGAGGTTCAGATATTAATAATTCATGTTCGA | 1467 |
| Dd | 1507 | CTTACCCCCCTGCAGCTTAAGTATGCAATCAAGCCGCTGTGTGTATGCGGTTCTTGATATCT | 1566 |
| QY | 1468 | AACCGAAGTTTAAGGAACGTTTAGCTCATATGATGTAAAAGTGTCAATTGACAACTAT | 1527 |
| Dd | 1567 | AAGCGAATTTCAAAGAGAGTCTGCCCATATATGATGTATGAGTATGAGCTCATTCGAAAGTAC | 1626 |
| QY | 1528 | TCTGCTGTGATCTGACACTGTGTGTAGATTAATAAAGCCTTCAACACAGCTGTGATCAA | 1587 |
| Dd | 1627 | TCGCTGGACACTTGTGATATGTTGTCTCCGCATCAAGAGCCTCGACAGCCAGAGTGGAGCAG | 1686 |
| QY | 1588 | ATTCTGTGAAAAAAGGGCAATACATCAGATTAAGAACAGCCGGAAGAGAAATAACAGCAGAA | 1647 |
| Dd | 1687 | ATTGTGGGGGGGGGCCCAACAATAACGATGAAGA-- -TGCACACCAAGGCCCGCAGCGGAA | 1743 |
| QY | 1648 | CATGAGACCAACAGATCTCAGATCTCGGTGCGGTGTCCAAGTTGAAAAACAGTA | 1707 |
| Dd | 1744 | ACGAGAGTGGCCCGAAGACCCAGCATATATGGGACGGCTTGGGAGTGGAGAAACAGGTC | 1803 |
| QY | 1708 | CAGTCCATAGAGTCCAAAGCTGAGCTGCCCTACTAGACATCTTTCAACAG | 1755 |
| Dd | 1804 | TTGTTCATGAAAAAGAGCTGCACCTTCTTGTGTGAGCATCTATACACAG | 1851 |

[illegible]

OY 664 TCAGTGGTTTATGCTACAGCAGGATTAATACAGCTGTGACATGATTTTGGT 723
Db 727 TCTGTGCTATGCTACAGCAGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
OY 724 CTATATTTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
Db 787 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
OY 784 ACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
Db 847 ACCTAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
OY 844 AAAATCTCCCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
Db 907 AAGTACCCCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 966
OY 904 TCTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
Db 967 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
OY 964 CAACACCCCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1023
Db 1027 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1086
OY 1024 GTTGGCTAGTTACGC 1040
Db 1087 GCCTGGAGATTTTACGC 1103

RESULT 8

US-09-177-650-1

Sequence 1, Application US/09177650

Patent No. 6413719

GENERAL INFORMATION:

APPLICANT: Leppert, Mark F.

APPLICANT: Singh, Nanda

TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE

TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)

FILE REFERENCE: 2323-134

CURRENT APPLICATION NUMBER: US/09/177,650

EARLIER FILING DATE: 1998-10-23

EARLIER APPLICATION NUMBER: 60/063,147

NUMBER OF SEQ ID NOS: 129

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 3232

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (128)..(2743)

FEATURE:

NAME/KEY: mutation

LOCATION: (975)..(976)

OTHER INFORMATION: There is an insertion of a GT between nucleotides

OTHER INFORMATION: 975 and 976 in kindred K1504.

FEATURE:

NAME/KEY: mutation

LOCATION: (978)

OTHER INFORMATION: The mutation A to G occurs at this base in kindred

OTHER INFORMATION: K3904.

FEATURE:

NAME/KEY: mutation

LOCATION: (1043)

OTHER INFORMATION: The mutation G to A occurs at this base in kindred

OTHER INFORMATION: K1705.

FEATURE:

NAME/KEY: mutation

LOCATION: (1691)..(1703)

OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are

OTHER INFORMATION: deleted in kindred K3369.

FEATURE:

NAME/KEY: allele

LOCATION: (1039)

OTHER INFORMATION: This polymorphism of C to T was seen in 7.0% of

OTHER INFORMATION: the control population.

FEATURE:

NAME/KEY: allele

LOCATION: (1846)

OTHER INFORMATION: This polymorphism of C to T was seen in 0.57% of

OTHER INFORMATION: the control population.

FEATURE:

NAME/KEY: mutation

LOCATION: (1469)

OTHER INFORMATION: The mutation C to T occurs at this base in kindred

OTHER INFORMATION: K1525.

FEATURE:

NAME/KEY: mutation

LOCATION: (1094)

OTHER INFORMATION: The mutation C to T occurs at this base in kindred

OTHER INFORMATION: K4443.

FEATURE:

NAME/KEY: mutation

LOCATION: (1125)

OTHER INFORMATION: The mutation G to A occurs at this base in kindred

OTHER INFORMATION: K4516.

FEATURE:

NAME/KEY: mutation

LOCATION: (2736)..(2737)

OTHER INFORMATION: There is an insertion of GGGC between these two

OTHER INFORMATION: nucleotides in K3963.

US-09-177-650-1

Query Match

Best Local Similarity 15.9%; Score 423.4; DB 4; Length 3232;

Matches 631; Conservative 0; Mismatches 346; Indels 0; Gaps 0;

OY 64 GGCCTGCTACTGCTGGGCGACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 123
Db 194 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253
OY 124 GAGACCCG 183
Db 254 GCGCGCTCGAGCG 313
OY 184 ACGAGTACCGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 243
Db 314 GCG 373
OY 244 AACGCTGAGAGACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 303
Db 374 AACGCTGAGAGCG 433
OY 304 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
Db 434 GTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
OY 364 TCAAGTTCCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
Db 494 GAGGCG 553
OY 424 ATTGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
Db 554 GTGCGATTCG 613
OY 484 TTGCTGGAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
Db 614 TTGCGCGGAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
OY 544 GTTCTGCAAAAACGAGGATATATTTTGCAGCGTGCAGTGCAGTGCAGTGCAGT 603
Db 674 CTGGCG 733

FILE REFERENCE: 3053-4052
 CURRENT APPLICATION NUMBER: US/09/105,058C
 CURRENT FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: US 60/055,599
 PRIOR FILING DATE: 1997-08-12
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: Patentln Ver. 2.1
 SEQ ID NO 3
 LENGTH: 900
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: 900 nucleotides of human KCNQ2
 US-09-105-058C-3

Query Match 15.8%; Score 421.4; DB 4; Length 900;
 Best Local Similarity 68.6%; Pred. No. 6e-115;
 Matches 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

194 AGAGCTGCGGCGCAAGTCAAGTACCGGGGTGAGAACTACCTGACAGCTGTGG 253
 17 AGCCCCCAAGCGCAAGCTTCTACGCAAGCTGAGAAATTCCTTACAGCTGTGG 76
 254 AGAGACCGCGGCGCTGGGGTTCATCACCACCGCTTTCCTTCTGCTGTGGTT 313
 77 AGCGGCGCGCGCTGGGCTTATCTACACGCTACGCTGCTTCTGCTGTGGTTCT 136
 314 GCTTATTTTGTGAGTGTCTTACCATCCCTGAGCAGACAAATTTGGCTCAAGTTGCC 373
 137 GCGTGTGCTGTGTGTGTTTCCACATCAAGAGATATGAGAGATCGGAGGGGCC 196
 374 TCTTATCTGAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 433
 197 TCTTATCTGAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 256
 434 GGTGCGGCGTGTGCTGTGCTGATATAGAGATGAGAGAGAGAGAGAGAGAGAG 493
 257 GGGCGCGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
 494 AGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
 317 AACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
 554 AACCTCAGGATATATTTTGGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
 377 GCTCCAGGAGACGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
 614 TCGCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
 437 TCGCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
 674 ATGCTCAGCAGCAAGATATATATACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 733
 497 ATGCGCAGCAGCAAGATATATATACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 556
 734 CGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 793
 557 CGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 616
 794 ATGCTCAGCAGCAAGATATATATACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 853
 617 ATGCTCAGCAGCAAGATATATATACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 676
 854 TAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 913
 677 AGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 973
 914 CACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 973
 737 CGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796
 974 AGAAGCACTTTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1033

Db 797 AGAAGCACTTTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
 QY 1034 GTTACGC 1040
 857 TTACGC 863

RESULT 11
 US-09-105-058C-5
 Sequence 5, Application US/09105058C
 Patent No. 6403360

GENERAL INFORMATION:
 APPLICANT: Blahar, Michael A.
 APPLICANT: Dworetzky, Steven
 APPLICANT: Gridkoff, Valentin K.
 APPLICANT: Levesque, Paul C.
 APPLICANT: Little, Wayne A.
 APPLICANT: Neubauer, Michael G.
 APPLICANT: Yang, Wen-Pin

TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 FILE REFERENCE: 3053-4052
 CURRENT APPLICATION NUMBER: US/09/105,058C
 CURRENT FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: US 60/055,599
 PRIOR FILING DATE: 1997-08-12
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: Patentln Ver. 2.1
 SEQ ID NO 5
 LENGTH: 900
 TYPE: DNA
 ORGANISM: mouse
 FEATURE:
 OTHER INFORMATION: 900 nucleotides of murine KCNQ2
 US-09-105-058C-5

Query Match 15.8%; Score 420.6; DB 4; Length 900;
 Best Local Similarity 68.7%; Pred. No. 1e-115;
 Matches 579; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 204 GCGCAGCTCAAGTACGCGGCGGTGAGAGTCTGATCAAGCTGTGAGAGAGAGAG 263
 Db 27 GCGCAGCGCTTCTACGCGCAAGCTGAGAAATTCCTTACAACTGTAGAGAGAGAG 86
 QY 264 CGGCTGCGGCTTCTACATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 323
 Db 87 CGGCTGCGGCTTCTACATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 146
 QY 324 GTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 383
 Db 147 TTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 206
 QY 384 GAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443
 Db 207 GCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266
 QY 444 TTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503
 Db 267 CTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
 QY 504 TGTAT 563
 Db 327 TGTAT 386
 QY 564 TAT 623
 Db 387 CATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 446
 QY 624 GCGCATGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 683
 Db 447 CGGTATGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 506
 QY 684 CAAGCAAT 743

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 15:52:52 ; Search time 93 Seconds
(without alignments)

Title: US-09-810-796-3
Perfect score: 2667

Sequence: 1 atgaagcatgtgagtcggy.....ctcatgtcaactgaataa 2667

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 778172

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Minimum DB seq length: 0
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Maximum DB seq length: 200000000000

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| | Maximum Match | 100% |

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Database : Published_Applications_MA.*
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14: /cgn2_6/plodata/2/pubnpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|---------------------|-------------------|
| 1 | 2667.2 | 100.0 | 2667 | 10 | US-09-810-796-3 | Sequence 3, Appl |
| 2 | 2662.2 | 99.8 | 2772 | 10 | US-09-825-147-1 | Sequence 1, Appl |
| 3 | 2662.2 | 99.8 | 3111 | 10 | US-09-825-147-3 | Sequence 3, Appl |
| 4 | 2630.2 | 98.6 | 2694 | 10 | US-09-810-796-2 | Sequence 2, Appl |
| 5 | 2626.4 | 98.5 | 3071 | 10 | US-09-810-796-1 | Sequence 1, Appl |
| 6 | 2617.2 | 98.1 | 3074 | 10 | US-09-813-148-1 | Sequence 1, Appl |
| 7 | 475.6 | 17.8 | 2169 | 9 | US-10-128-870-22 | Sequence 22, Appl |
| 8 | 465.4 | 17.5 | 896 | 9 | US-10-128-870-1 | Sequence 1, Appl |
| 9 | 427.2 | 16.0 | 2565 | 9 | US-10-128-870-26 | Sequence 26, Appl |
| 10 | 425.1 | 15.9 | 3287 | 9 | US-10-128-870-19 | Sequence 19, Appl |
| 11 | 421.4 | 15.8 | 900 | 9 | US-10-128-870-3 | Sequence 3, Appl |
| 12 | 420.6 | 15.8 | 900 | 9 | US-10-128-870-5 | Sequence 5, Appl |
| 13 | 363.8 | 13.6 | 930 | 9 | US-10-128-870-17 | Sequence 17, Appl |
| 14 | 334.2 | 12.5 | 735 | 9 | US-10-128-870-7 | Sequence 7, Appl |
| 15 | 267.8 | 10.0 | 2028 | 10 | US-09-840-125-1 | Sequence 1, Appl |
| 16 | 266.6 | 10.0 | 2821 | 10 | US-09-880-107-3358 | Sequence 3358, A |
| 17 | 130.4 | 4.9 | 416 | 10 | US-09-960-352-13343 | Sequence 13343, A |
| 18 | 104.2 | 3.9 | 429 | 10 | US-09-783-590-4509 | Sequence 4509, A |
| 19 | 58.4 | 2.2 | 777 | 9 | US-09-985-920-7 | Sequence 7, Appl |

| | | | | | | | |
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| C | 20 | 58.4 | 2.2 | 1278 | 9 | US-10-016-647-1 | Sequence 1, Appl |
| C | 21 | 58.4 | 2.2 | 1844 | 9 | US-10-016-647-3 | Sequence 3, Appl |
| C | 22 | 51.8 | 1.9 | 998 | 10 | US-09-864-761-1804 | Sequence 1804, Ap |
| C | 23 | 51.8 | 1.9 | 1340 | 10 | US-09-864-761-20550 | Sequence 20550, A |
| C | 24 | 51.8 | 1.9 | 1979 | 10 | US-09-864-761-3784 | Sequence 3784, Ap |
| C | 25 | 46.6 | 1.8 | 249487 | 9 | US-10-026-188-3 | Sequence 3, Appl |
| C | 26 | 48.4 | 1.7 | 911 | 9 | US-09-989-920-8 | Sequence 8, Appl |
| C | 27 | 43.8 | 1.6 | 494 | 10 | US-09-925-297-153 | Sequence 153, App |
| C | 28 | 42.8 | 1.6 | 226 | 9 | US-10-128-870-9 | Sequence 9, Appl |
| C | 29 | 41.2 | 1.5 | 410 | 9 | US-09-854-133-400 | Sequence 400, App |
| C | 30 | 41.2 | 1.5 | 410 | 10 | US-09-758-973-400 | Sequence 400, App |
| C | 31 | 41.2 | 1.5 | 8459 | 10 | US-09-817-913-8 | Sequence 8, Appl |
| C | 32 | 41.2 | 1.5 | 8459 | 10 | US-09-817-913-8 | Sequence 8, Appl |
| C | 33 | 40.6 | 1.5 | 1506 | 10 | US-09-963-285-9 | Sequence 9, Appl |
| C | 34 | 40.6 | 1.5 | 3289 | 10 | US-09-963-285-8 | Sequence 8, Appl |
| C | 35 | 40.6 | 1.5 | 4158 | 10 | US-09-963-285-3 | Sequence 3, Appl |
| C | 36 | 40.6 | 1.5 | 6458 | 10 | US-09-963-285-1 | Sequence 1, Appl |
| C | 37 | 39.2 | 1.5 | 369 | 10 | US-09-757-781-57 | Sequence 57, Appl |
| C | 38 | 39.2 | 1.5 | 383 | 10 | US-09-070-927A-689 | Sequence 689, App |
| C | 39 | 39.2 | 1.5 | 2968 | 10 | US-09-757-781-3 | Sequence 3, Appl |
| C | 40 | 39.2 | 1.5 | 3700 | 10 | US-09-303-332-3 | Sequence 3, Appl |
| C | 41 | 38.8 | 1.5 | 1503 | 10 | US-09-815-242-7680 | Sequence 7680, Ap |
| C | 42 | 38.8 | 1.5 | 1533 | 10 | US-09-815-242-7755 | Sequence 7755, Ap |
| C | 43 | 38.6 | 1.4 | 1326 | 10 | US-09-749-728B-12 | Sequence 12, Appl |
| C | 44 | 38.4 | 1.4 | 1224 | 10 | US-09-972-529-1 | Sequence 1, Appl |
| C | 45 | 38.4 | 1.4 | 3192 | 10 | US-09-788-654A-1 | Sequence 1, Appl |

ALIGNMENTS

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RESULT 1
US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICGen, Inc.
; TITLE OF INVENTION: KCNO5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNO5-2 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCNO5-2
US-09-810-796-3

Query Match      100.0%; Score 2667; DB 10; Length 2667;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | |
|----|-----|--|-----|
| QY | 1 | ATGAAGATGTGAGATCGGGGCGAGGGTGGCTGGACTGGCAGCGCCAGGGG | 60 |
| Db | 1 | ATGAAGATGTGAGATCGGGCGAGGGTGGCTGGACTGGCAGCGCCAGGGG | 60 |
| QY | 61 | GACGGCTCTACTCTGGCACCGCCGGCCACGCTTGGTGGCGGCGGCGTGGCTG | 120 |
| Db | 61 | GACGGCTCTACTCTGGCACCGCCGGCCACGCTTGGTGGCGGCGGCGTGGCTG | 120 |
| QY | 121 | ACGCAAGCGCCGCGGCGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAACCGCTCT | 180 |
| Db | 121 | ACGCAAGCGCCGCGGCGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAACCGCTCT | 180 |

| | | | |
|----|------|---|------|
| QY | 181 | TACACGAGTACCCAGAGCTGCGGCGCAACGTCAGTACCGGGGGTGCAGAACTACTG | 240 |
| Db | 181 | TACACGAGTACCCAGAGCTGCGGCGCAACGTCAGTACCGGGGGTGCAGAACTACTG | 240 |
| QY | 241 | TACACGAGTACCCAGAGCTGCGGCGCAACGTCAGTACCGGGGGTGCAGAACTACTG | 300 |
| Db | 241 | TACACGAGTACCCAGAGCTGCGGCGCAACGTCAGTACCGGGGGTGCAGAACTACTG | 300 |
| QY | 301 | CTGTCTTGGTGGTGTGATTTTGTACAGTTTTCACATCCCTGAGCACAAAAATGG | 360 |
| Db | 301 | CTGTCTTGGTGGTGTGATTTTGTACAGTTTTCACATCCCTGAGCACAAAAATGG | 360 |
| QY | 361 | GCCTCAAGTGGCCTCTGATCCCTGGAGTTCGTATGCTCTTGGTGGAGTTC | 420 |
| Db | 361 | GCCTCAAGTGGCCTCTGATCCCTGGAGTTCGTATGCTCTTGGTGGAGTTC | 420 |
| QY | 421 | ATCATTCGATCTGCTGCTCGGGTTCCTGTTCGATATAGAGGATGGCAAGAGACTG | 480 |
| Db | 421 | ATCATTCGATCTGCTGCTCGGGTTCCTGTTCGATATAGAGGATGGCAAGAGACTG | 480 |
| QY | 481 | AGGTTTGCCTGAAAGCCCTTCTGTGTATAGATACCATTGTTCTTATCGCTTCAATAGCA | 540 |
| Db | 481 | AGGTTTGCCTGAAAGCCCTTCTGTGTATAGATACCATTGTTCTTATCGCTTCAATAGCA | 540 |
| QY | 541 | GTTCCTTTCGCAAAAACCTCAGGGTATATTTTGGCAGCTCGCACTAGAACTCCGT | 600 |
| Db | 541 | GTTCCTTTCGCAAAAACCTCAGGGTATATTTTGGCAGCTCGCACTAGAACTCCGT | 600 |
| QY | 601 | TTCCTACAGATCTCCCGCATGGTGCATGACGCCAAGGGAGGCACATGGAAATTACTG | 660 |
| Db | 601 | TTCCTACAGATCTCCCGCATGGTGCATGACGCCAAGGGAGGCACATGGAAATTACTG | 660 |
| QY | 661 | GATTAGAGGTTTATGTCACAGCAAGGAATTAATCACAGCTGGTACATAGAGATTTTG | 720 |
| Db | 661 | GATTAGAGGTTTATGTCACAGCAAGGAATTAATCACAGCTGGTACATAGAGATTTTG | 720 |
| QY | 721 | GTTCTTATTTTGGCTCTTCTCTGTCTATCTGTGGAAAAAGATCCCAATAAAGAGTTT | 780 |
| Db | 721 | GTTCTTATTTTGGCTCTTCTCTGTCTATCTGTGGAAAAAGATCCCAATAAAGAGTTT | 780 |
| QY | 781 | TCTACATTTGAGAGATGCTCTCGGGGGGGGCAATTAATGACAACTATTTGGCTATGGA | 840 |
| Db | 781 | TCTACATTTGAGAGATGCTCTCGGGGGGGGCAATTAATGACAACTATTTGGCTATGGA | 840 |
| QY | 841 | GACAAACCTCCCTAACCTTGGCTGGGAAGATTGTTCTCGAGGCTTTCGACTCTTGGC | 900 |
| Db | 841 | GACAAACCTCCCTAACCTTGGCTGGGAAGATTGTTCTCGAGGCTTTCGACTCTTGGC | 900 |
| QY | 901 | ATTCTCTTCTTGGACCTTCTGCGCGCATTTCTTGGCTCAGGTTTTCGATTAAAAAGTACAA | 960 |
| Db | 901 | ATTCTCTTCTTGGACCTTCTGCGCGCATTTCTTGGCTCAGGTTTTCGATTAAAAAGTACAA | 960 |
| QY | 961 | GAACACACCGCCGGAAGAACTTTGAAAAAGAAAGAACCGAGTGGCAACCTCATTTACG | 1020 |
| Db | 961 | GAACACACCGCCGGAAGAACTTTGAAAAAGAAAGAACCGAGTGGCAACCTCATTTACG | 1020 |
| QY | 1021 | TGTGTGTTGGCTGACTTACGACGCTGATGAGAAAACTGTTCATTTGCAATCGAACCTGGAAACCA | 1080 |
| Db | 1021 | TGTGTGTTGGCTGACTTACGACGCTGATGAGAAAACTGTTCATTTGCAATCGAACCTGGAAACCA | 1080 |
| QY | 1081 | CACCTTGAAGGCTTGGACACACTCGAGCCCTACCAATTCAGAACTAAAGTTTAAAGAGCGA | 1140 |
| Db | 1081 | CACCTTGAAGGCTTGGACACACTCGAGCCCTACCAATTCAGAACTAAAGTTTAAAGAGCGA | 1140 |
| QY | 1141 | GTCGCGATGCTAGCCCAAGGGCCAGAGATTAAAGCCGGAACGCTCAGTAAAGTGAAC | 1200 |
| Db | 1141 | GTCGCGATGCTAGCCCAAGGGCCAGAGATTAAAGCCGGAACGCTCAGTAAAGTGAAC | 1200 |
| QY | 1201 | AGGAGTCCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCACCAAGATGCGAAGAGAC | 1260 |
| Db | 1201 | AGGAGTCCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCACCAAGATGCGAAGAGAC | 1260 |

| | | | |
|----|------|---|------|
| QY | 1261 | IIIIIGAGGCTTCAAGACCGGAACCCGGCTTCGGCCCTCGCTGCGCTCTCAAAAGTTCAGCCA | 1320 |
| Db | 1261 | TGGAGCTTCAAGACCGGAACCCGGCTTCGGCCCTCGCTGCGCTCTCAAAAGTTCAGCCA | 1320 |
| QY | 1321 | AAACCAAGTATGATGCTGACACACCCCTTGGACACTGATGATATGATGAAAAAGGA | 1380 |
| Db | 1321 | AAACCAAGTATGATGCTGACACACCCCTTGGACACTGATGATATGATGAAAAAGGA | 1380 |
| QY | 1381 | TGCCAGTGTGATGTATCAAGTGGAAAGCCTCACCCACCACCTTAAAGTGTATTCGAGCT | 1440 |
| Db | 1381 | TGCCAGTGTGATGTATCAAGTGGAAAGCCTCACCCACCACCTTAAAGTGTATTCGAGCT | 1440 |
| QY | 1441 | ATCAAAATTAAGAATTTCACTTGGCAAAAGGAAGTTAAGAAACGTTACGTCATAT | 1500 |
| Db | 1441 | ATCAAAATTAAGAATTTCACTTGGCAAAAGGAAGTTAAGAAACGTTACGTCATAT | 1500 |
| QY | 1501 | GATGTAAAGATGTGATTAAGCAAAATATTTCTGCTGCTATGTCAGCATGTTGTAGAAAT | 1560 |
| Db | 1501 | GATGTAAAGATGTGATTAAGCAAAATATTTCTGCTGCTATGTCAGCATGTTGTAGAAAT | 1560 |
| QY | 1561 | AAAAGCCTTCAACACCGTGTGATCAAAATTCCTGGAAAAGGCAAAATCACATAGATAG | 1620 |
| Db | 1561 | AAAAGCCTTCAACACCGTGTGATCAAAATTCCTGGAAAAGGCAAAATCACATAGATAG | 1620 |
| QY | 1621 | AAGAGCCGAGAGAAAATPACAGCAGAACATGAGACCACACAGCATCTCAATATGCTGGT | 1680 |
| Db | 1621 | AAGAGCCGAGAGAAAATPACAGCAGAACATGAGACCACACAGCATCTCAATATGCTGGT | 1680 |
| QY | 1681 | CGGGTGTGTCAAGGTGTGAAAAACAGGTACAGTCCATAGAGTCCACGCTGACCTCCACTA | 1740 |
| Db | 1681 | CGGGTGTGTCAAGGTGTGAAAAACAGGTACAGTCCATAGAGTCCACGCTGACCTCCACTA | 1740 |
| QY | 1741 | GACATCTATCAACAGTTCCTTGGAAAAGCTCTGCGCCACCCCTCGCTTGGCTTCAATTC | 1800 |
| Db | 1741 | GACATCTATCAACAGTTCCTTGGAAAAGCTCTGCGCCACCCCTCGCTTGGCTTCAATTC | 1800 |
| QY | 1801 | CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA | 1860 |
| Db | 1801 | CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA | 1860 |
| QY | 1861 | GATCTTTCGGGTTCCGCACAAAACAGGGGTGCTTATCCAGATCAACTGTGCGCAATTC | 1920 |
| Db | 1861 | GATCTTTCGGGTTCCGCACAAAACAGGGGTGCTTATCCAGATCAACTGTGCGCAATTC | 1920 |
| QY | 1921 | TGCAGAGGCTGCAATTCATCTGAGCGCCAAATGAGTTCAGTCCAGACTTCTTACGGG | 1980 |
| Db | 1921 | TGCAGAGGCTGCAATTCATCTGAGCGCCAAATGAGTTCAGTCCAGACTTCTTACGGG | 1980 |
| QY | 1981 | CTTAGGCCCTACTGTGCACAGTCAAGCAACAGGTGCCAATTAAGTCAAAAGCATGGCTCA | 2040 |
| Db | 1981 | CTTAGGCCCTACTGTGCACAGTCAAGCAACAGGTGCCAATTAAGTCAAAAGCATGGCTCA | 2040 |
| QY | 2041 | GCAGTGGCAGCCAAACCAATTTGCAAAACCAATTAATAGCGCACCCAGCAGCAGCAGC | 2100 |
| Db | 2041 | GCAGTGGCAGCCAAACCAATTTGCAAAACCAATTAATAGCGCACCCAGCAGCAGCAGC | 2100 |
| QY | 2101 | CCAAACAATTTACAGTTCACCACCTCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAA | 2160 |
| Db | 2101 | CCAAACAATTTACAGTTCACCACCTCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAA | 2160 |
| QY | 2161 | ACTGTGCACCTTAACCCCTGCAGGCTTACAGGAAGCATTTCTGAGAGTACACCACTGGCTT | 2220 |
| Db | 2161 | ACTGTGCACCTTAACCCCTGCAGGCTTACAGGAAGCATTTCTGAGAGTACACCACTGGCTT | 2220 |
| QY | 2221 | GTTTGCCTCCAGGAATAATGTTCAAGTTGACAGTCAAAATTCACCAAGCAGCTTCTATG | 2280 |
| Db | 2221 | GTTTGCCTCCAGGAATAATGTTCAAGTTGACAGTCAAAATTCACCAAGCAGCTTCTATG | 2280 |
| QY | 2281 | AGGAAGAAGTTTGAATGGGAGAGAAACTCTGTTGTCTGTCTCTCCATGCTGCCGAAG | 2340 |
| Db | 2281 | AGGAAGAAGTTTGAATGGGAGAGAAACTCTGTTGTCTGTCTCTCCATGCTGCCGAAG | 2340 |
| QY | 2341 | GACTTGGGCAAAATCTTGTCTGTGCAAAACTGATCAAGGTGACCTGAGGAATCAATATA | 2400 |


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Db 2341 GACTTGGGCAATCTTTTGTGTGTAAGCAACCTGATCGACCTGACCGAGSAGTGAATATA 2400
OY 2401 CACCTTTCAGGAGAGTGAAGTCAAGTGGCTCAGAGAGCAGCAGATTTTACCCTAAATGG 2460
Db 2401 CACCTTTCAGGAGAGTGAAGTGGCTCAGAGAGCAGCAGATTTTACCCTAAATGG 2460
OY 2461 AGGGAATCCAAATTTGTTTAACTGATCAAGAGTGGTCCCGAGAGAGCAGAGACAGAC 2520
Db 2461 AGGGAATCCAAATTTGTTTAACTGATCAAGAGTGGTCCCGAGAGAGCAGAGACAGAC 2520
OY 2521 ACTTTGATGCGCGACCGGAGCTCCAGAGAAAGTTCCTTTCATCAGACTCTTAAG 2580
Db 2521 ACTTTGATGCGCGACCGGAGCTCCAGAGAAAGTTCCTTTCATCAGACTCTTAAG 2580
OY 2581 ACTGGAAGTCAAGATCACTCAGACCAATTTTGAAGCAGAGAAAGTCAAGTGGCTTC 2640
Db 2581 ACTGGAAGTCAAGATCACTCAGACCAATTTTGAAGCAGAGAAAGTCAAGTGGCTTC 2640
OY 2641 AGCTTGCCTCATGTCGAACGGAATATA 2667
Db 2641 AGCTTGCCTCATGTCGAACGGAATATA 2667

RESULT 2
US-09-825-147-1
Sequence 1, Application US/09825147
Patent No. US20020042505A1
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael C.
APPLICANT: Friederich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
FILE REFERENCE: LEX-0160-USA
CURRENT APPLICATION NUMBER: US/09/825,147
PRIORITY FILING DATE: 2001-04-03
CURRENT APPLICATION NUMBER: US 60/194,255
PRIORITY FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2772
TYPE: DNA
ORGANISM: homo sapiens
US-09-825-147-1

Query Match 99.8% Score 2662.2: DB 10: Length 2772:
Best Local Similarity 99.9%: Pred. No. 0:
Matches 2664: Conservative 0: Mismatches 3: Indels 0: Gaps 0:
OY 1 ATGAAGAGTGTGGAGTGGGCGCGGAGAGTGTCTGTGAAGTGTGGAGCGCGGAGGCG 60
Db 106 ATGAAGAGTGTGGAGTGGGCGCGGAGAGTGTCTGTGAAGTGTGGAGCGCGGAGGCG 165
OY 61 GACGGCTGTCTACTGTGGGACCGCGCGGCGGACGCTTGTGTGGCGGCGGCGGCGCTG 120
Db 166 GACGGCTGTCTACTGTGGGACCGCGCGGCGGACGCTTGTGTGGCGGCGGCGGCGCTG 225
OY 121 AGGGAAGCGCGCGGCGGAGAGCGAGGAGCGGAGTGAAGTGTGGGAGAGCGCGCTCT 180
Db 226 AGGGAAGCGCGCGGCGGAGAGCGAGGAGCGGAGTGAAGTGTGGGAGAGCGCGCTCT 285
OY 181 TACACGAGTACGACAGCTGCGCGGCGGACGTCAGTACGCGGCGGCTGACAACTACCTG 240
Db 286 TACACGAGTACGACAGCTGCGCGGCGGACGTCAGTACGCGGCGGCTGACAACTACCTG 345
OY 241 TACACGAGTACGACAGCTGCGCGGCGGCTGACCTACGAGCTTGTGTTTCTC 300

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Db 346 TACACGAGTACGACAGCTGCGCGGCGGAGTGTGATCTACACGCTTGTGTTTCTC 405
OY 301 CTGTGCTTTGGTTCCTGATTTTTCAGAGTGTTCATCATCCCTGAGCAGCAAAATGG 360
Db 406 CTGTGCTTTGGTTCCTGATTTTTCAGAGTGTTCATCATCCCTGAGCAGCAAAATGG 465
OY 361 GCCTCAAGTGTGCTGTGATCCGAGTTCGAGTATGATGATGCTGTTGTTGGAGTTTC 420
Db 466 GCCTCAAGTGTGCTGTGATCCGAGTTCGAGTATGATGATGATGCTGTTGTTGGAGTTTC 525
OY 421 ATCATTCGAATCTGTCTGTGCGGAGTTCCTGTTATGATATACATGTTTCTTATCGCTCA 540
Db 526 ATCATTCGAATCTGTCTGTGCGGAGTTCCTGTTATGATATGATGATGATGATGATGAT 585
OY 481 AGTTTGTCTGGAAGCGCTTCTGTGTTATGATATACATGTTTCTTATCGCTCA 645
Db 586 AGTTTGTCTGGAAGCGCTTCTGTGTTATGATATACATGTTTCTTATCGCTCA 645
OY 541 GTTGTTCCTGCAAAACTCAGAGTAAATTTTGGCAGCTGTGACACAGAGTTCGCT 600
Db 646 GTTGTTCCTGCAAAACTCAGAGTAAATTTTGGCAGCTGTGACACAGAGTTCGCT 705
OY 601 TTCTACAGATCTCCGCGATGCTGCGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 706 TTCTACAGATCTCCGCGATGCTGCGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 765
OY 661 GGTTCAGTGTGTTATGCTCAGCAGCAGAGGATTAATCAGCTGTTGATATGATTTTTC 720
Db 766 GGTTCAGTGTGTTATGCTCAGCAGCAGAGGATTAATCAGCTGTTGATATGATTTTTC 825
OY 721 GTTCTATTTTTCCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db 826 GTTCTATTTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 885
OY 781 TCTACATATGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 886 TCTACATATGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 945
OY 841 GACAAACCTCCCTAACTTGTGCTGAGAGATGCTTCTGCGAGGCTTTCGACCTCTGTC 900
Db 946 GACAAACCTCCCTAACTTGTGCTGAGAGATGCTTCTGCGAGGCTTTCGACCTCTGTC 1005
OY 901 ATTTCTCTTGTGACCTTCTGCGGATCTTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTG 960
Db 1006 ATTTCTCTTGTGACCTTCTGCGGATCTTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTG 1065
OY 961 GAACAACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db 1066 GAACAACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1125
OY 1021 TGTGTTTGGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Db 1126 TGTGTTTGGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1185
OY 1081 CACTTGAAGGCTTGTGACCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 1186 CACTTGAAGGCTTGTGACCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1245
OY 1141 GTGCGCATGCTGACCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Db 1246 GTGCGCATGCTGACCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1305
OY 1201 AGGAGGCTCCCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Db 1306 AGGAGGCTCCCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1365
OY 1261 TGAAGCTTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Db 1366 TGAAGCTTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1425
OY 1321 AAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 1426 AAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1485

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Db 525 GCGTCAGTGGCTCTTATCTCTGAGTTCGATGATGATGCTGCTGTTGGTGGCTC 584
OY 421 ATCATTCGATCTGCTGCGGGTCTGCTGTGTCATATAGAGATGGACGAACACAGC 480
Db 585 ATCATTCGATCTGCTGCGGGTCTGCTGTGTCATATAGAGATGGACGAACACAGC 644
OY 481 AGTTTGGTCGAAGACCCCTCTGTGTATATAGATACCATTTGCTTATGCTTCAATAGCA 540
Db 645 AGTTTGGTCGAAGACCCCTCTGTGTATATAGATACCATTTGCTTATGCTTCAATAGCA 704
OY 541 GTTGTTCGCAAAAACCTCAGGGTAAATATTTTCCACGCTGACCTCAGAACTCCGT 600
Db 705 GTTGTTCGCAAAAACCTCAGGGTAAATATTTTCCACGCTGACCTCAGAACTCCGT 764
OY 601 TTCCATACAGATCTCCGCAATGCTGGCGATGACCGGAAGGGGGGCGCTGGAATATAGC 660
Db 765 TTCCATACAGATCTCCGCAATGCTGGCGATGACCGGAAGGGGGGCGCTGGAATATAGC 824
OY 661 GGTTCAGTGGTTATGCTACAGCAAGAAATTAATCAGACTTGGTATAGAGATTTTGG 720
Db 825 GGTTCAGTGGTTATGCTACAGCAAGAAATTAATCAGACTTGGTATAGAGATTTTGG 884
OY 721 GTTCTTATTTTTCGCTCTTCTTCTATCTGTGTGTAATGGAAGAGATGCCAATAAGATT 780
Db 885 GTTCTTATTTTTCGCTCTTCTTCTATCTGTGTGTAATGGAAGAGATGCCAATAAGATT 944
OY 781 TCCATATATGCAAGATCTCTGTGGGGGACATATACATGACACTTGGCTATAGCA 840
Db 945 TCCATATATGCAAGATCTCTGTGGGGGACATATACATGACACTTGGCTATAGCA 1004
OY 841 GACAAACCTCCCTACTGCTGGGGAAGATTGCTTTCGCAAGCTTTCACCTCCTTGGC 900
Db 1005 GACAAACCTCCCTACTGCTGGGGAAGATTGCTTTCGCAAGCTTTCACCTCCTTGGC 1064
OY 901 ATTTCTTTCTTTGCACTTCTCTGCGGCATTTCTTGGCTCAGGTTTTCATTTAAAGTACAA 960
Db 1065 ATTTCTTTCTTTGCACTTCTCTGCGGCATTTCTTGGCTCAGGTTTTCATTTAAAGTACAA 1124
OY 961 GAAACAACCCGCGAGAAACACTTTGAGAAAGAAAGAACCCAGCTCCCAACCTCATTCAG 1020
Db 1125 GAAACAACCCGCGAGAAACACTTTGAGAAAGAAAGAACCCAGCTCCCAACCTCATTCAG 1184
OY 1021 TGTGTTGGCGTAGTTAGCAGCTGATGAGAAATCTGTTTCATTCACCTGGAAGCCA 1080
Db 1185 TGTGTTGGCGTAGTTAGCAGCTGATGAGAAATCTGTTTCATTCACCTGGAAGCCA 1244
OY 1081 CACTTGAAGGCTTGCACACTGACAGCTTACCAATCAGAACTAAGTTTAAAGAGCCA 1140
Db 1245 CACTTGAAGGCTTGCACACTGACAGCTTACCAATCAGAACTAAGTTTAAAGAGCCA 1304
OY 1141 GTGCGATGGCTAGCCCGAGGGGCGAGAGTATTAAGAGCGCAAGCTCAGTAAAGTAC 1200
Db 1305 GTGCGATGGCTAGCCCGAGGGGCGAGAGTATTAAGAGCGCAAGCTCAGTAAAGTAC 1364
OY 1201 AGAGAGTCCCAAGACGACGACATCAGCGGAGGAGCTCCCAACAAAGTGCAGAAAGAGC 1260
Db 1365 AGAGAGTCCCAAGACGACGACATCAGCGGAGGAGCTCCCAACAAAGTGCAGAAAGAGC 1424
OY 1261 TGGAGTTTCAACGACCGGAACCCGCTTCCGCGCTCGCTGGGCTCAAAACTTCTCAGCCA 1320
Db 1425 TGGAGTTTCAACGACCGGAACCCGCTTCCGCGCTCGCTGGGCTCAAAACTTCTCAGCCA 1484
OY 1321 AAACAGTATAGATGCTGACACAGCGCTTGGCATGATGATATATGATGGAAGAAAGGA 1380
Db 1485 AAACAGTATAGATGCTGACACAGCGCTTGGCATGATGATATATGATGGAAGAAAGGA 1544
OY 1381 TGCAGTGTGATGTATACGTGAGAGACCTTACCCGACACTTAAACTGTCTATTCAGCT 1440
Db 1545 TGCAGTGTGATGTATACGTGAGAGACCTTACCCGACACTTAAACTGTCTATTCAGCT 1504
OY 1441 ATCAGATTTATGAATTTTCACTGTTGCAAAAGGAAGTTTAAAGAAACCTTACGCTCAT 1500
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Db 1605 ATCAGATTTATGAATTTTCACTGTTGCAAAAAGCAAGCTTTAAAGAAACCTTACGCTCATAT 1664
OY 1501 GATGTAAAGATGCTCATTTGAACAATATTTCTGCTGTCATCTGACATGTTGTGTAGAAAT 1560
Db 1665 GATGTAAAGATGCTCATTTGAACAATATTTCTGCTGTCATCTGACATGTTGTGTAGAAAT 1724
OY 1561 AAAAGCTTCAAAACACGCTGTGATCAAAATTTCTTGGAAAAGGGCAATTCACATACATTAAG 1620
Db 1725 AAAAGCTTCAAAACACGCTGTGATCAAAATTTCTTGGAAAAGGGCAATTCACATACATTAAG 1784
OY 1621 AAGAGCGAGAGAAATTAACAGAGAAACATGAGACACAGACATCTCAGTATAGCGGT 1680
Db 1785 AAGAGCGAGAGAAATTAACAGAGAAACATGAGACACAGAGATCTCAGTATAGCGGT 1844
OY 1681 CGGAGGTCAAGGTTGAAAAAAGAGTACAGTCAATGAGTCCAAAGCTGACCTCACTA 1740
Db 1845 CGGAGGTCAAGGTTGAAAAAAGAGTACAGTCAATGAGTCCAAAGCTGACCTCACTA 1904
OY 1741 GACATCTATCAACAGGTCCTTGGAAAAGGCTGCTCAGCCCTGCTTGGCTTCACTT 1800
Db 1905 GACATCTATCAACAGGTCCTTGGAAAAGGCTGCTCAGCCCTGCTTGGCTTCACTT 1964
OY 1801 CAGATCCGACCTTTTGAATGTGAAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA 1860
Db 1965 CAGATCCGACCTTTTGAATGTGAAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA 2024
OY 1861 GATCTTTCGGGTTCCGACAAAACAGTGGCTGTATCCAGATCAACTAGTGGCAACATC 1920
Db 2025 GATCTTTCGGGTTCCGACAAAACAGTGGCTGTATCCAGATCAACTAGTGGCAACATC 2084
OY 1921 TCGAGAGGCTTCGACATTTCTGACGCGCAATATGATTCAGTCCGACACTTCTACGCG 1980
Db 2085 TCGAGAGGCTTCGACATTTCTGACGCGCAATATGATTCAGTCCGACACTTCTACGCG 2144
OY 1981 CTTAGCCCTACTATGACACATCAATCAAGAACACAGGTGCAATTTGTAAGCCGATGGCTCA 2040
Db 2145 CTTAGCCCTACTATGACACATCAATCAAGAACACAGGTGCAATTTGTAAGCCGATGGCTCA 2204
OY 2041 GCAGTGGCAGCCCAACACACATTTGCAAAACCAATTAATACGGGACCCCAAGCAGCAGCC 2100
Db 2205 GCAGTGGCAGCCCAACACACATTTGCAAAACCAATTAATACGGGACCCCAAGCAGCAGCC 2264
OY 2101 CCAACAACCTTTACAGATTCACACTCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAA 2160
Db 2265 CCAACAACCTTTACAGATTCACACTCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAA 2324
OY 2161 ACCTGCAACCTTAACCTTGAAGGCTTACAGAAAGCAATTTCTGACGTCACACACTGCTT 2220
Db 2325 ACCTGCAACCTTAACCTTGAAGGCTTACAGAAAGCAATTTCTGACGTCACACACTGCTT 2384
OY 2221 GTTGCCTCCCAAGGAAATGTTCAAGTTGCAAGTCAATCTCACCAAGGACCCGTTATG 2280
Db 2385 GTTGCCTCCCAAGGAAATGTTCAAGTTGCAAGTCAATCTCACCAAGGACCCGTTATG 2444
OY 2281 AGGAAAGCTTTGACATGAGAGAGAAACTGTGTCTGTCTGTCTGCCATGTGTGCCAAG 2340
Db 2445 AGGAAAGCTTTGACATGAGAGAGAAACTGTGTCTGTCTGTCTGCCATGTGTGCCAAG 2504
OY 2241 GACTTGGGCAAAATCTTGTGTGCAAAACCTGATCAGTGCACCGAGAACTGAATATA 2400
Db 2505 GACTTGGGCAAAATCTTGTGTGCAAAACCTGATCAGTGCACCGAGAACTGAATATA 2564
OY 2401 CAACCTTCAGGAGAGTGAAGTCAAGTGGCTCCAGAGGACCAAGATTTTAAACCCAAATGG 2460
Db 2565 CAACCTTCAGGAGAGTGAAGTCAAGTGGCTCCAGAGGACCAAGATTTTAAACCCAAATGG 2624
OY 2461 AGGGAATCCAAATTTGTTATATACATGATGAAGAGTGGTCCGAGAGACAGATACAGAC 2520
Db 2625 AGGGAATCCAAATTTGTTATATACATGATGAAGAGTGGTCCGAGAGACAGATACAGAC 2684
OY 2521 ACTTTGATGCTCGGACGCGAGCCGTCAGGAGAACTCCCTTTGGATCAGACTGCTTAAAG 2580
Db 2685 ACTTTGATGCTCGGACGCGAGCCGTCAGGAGAACTCCCTTTGGATCAGACTGCTTAAAG 2744
|||||

QY 2581 ACTGGAAGTCAATCATCTCAGACGATTTGTAAAGCAGAGAAAGTACAGATGCCCTC 2640
DB 2745 ACTGGAAGTCAATCATCTCAGACGATTTGTAAAGCAGAGAAAGTACAGATGCCCTC 2804
QY 2641 AGCTTGCCCTCAATGTCAAACTGAAATAA 2667
DB 2805 AGCTTGCCCTCAATGTCAAACTGAAATAA 2831

RESULT 4

US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: IGen, Inc.
; TITLE OF INVENTION: KCM05, a No. US20020102677A1e1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCM05-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)-(2694)
; OTHER INFORMATION: KCM05-1
US-09-810-796-2

Query Match 98.6%; Score 2630; DB 10; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 1 ATGGAAGATGTGGAGTGGGCGGCGGAGGGTGTCTGTAAGTCCGCGCAGGGGC 60
DB 1 ATGGAAGATGTGGAGTGGGCGGCGGAGGGTGTCTGTAAGTCCGCGCAGGGGC 60
QY 61 GAGGCGCTGCTACTGCTGGGCGACCGCGGCGCAGGCTGTGGGCGGCGGCTGG 120
DB 61 GAGGCGCTGCTACTGCTGGGCGACCGCGGCGCAGGCTGTGGGCGGCGGCTGG 120
QY 121 AGGGAAGCCCGCGGCGAAGCAGAGGGGCGCGGATGAGCTGTGGGGAAGCGCTCT 180
DB 121 AGGGAAGCCCGCGGCGAAGCAGAGGGGCGCGGATGAGCTGTGGGGAAGCGCTCT 180
QY 181 TACACGAGTACGACGAGCTGCCGCGCAAGTCAAGTACCGCGGCGGTGACAACTAC 240
DB 181 TACACGAGTACGACGAGCTGCCGCGCAAGTCAAGTACCGCGGCGGTGACAACTAC 240
QY 241 TACACGAGTACGAGACCGCGGCGGTGAGTCAATCAACAGCGTGTGCTTTTCTC 300
DB 241 TACACGAGTACGAGACCGCGGCGGTGAGTCAATCAACAGCGTGTGCTTTTCTC 300
QY 301 CTGTGCTTGGTGTGCTGATTTGTCAAGTGTCTTCTACCAATCCCTGAGACACAAAT 360
DB 301 CTGTGCTTGGTGTGCTGATTTGTCAAGTGTCTTCTACCAATCCCTGAGACACAAAT 360
QY 361 GCCTCAAGTGTGCTGATCTGAGATGCTGATGATGCTGCTTGTGAGTTC 420
DB 361 GCCTCAAGTGTGCTGATCTGAGATGCTGATGATGCTGCTTGTGAGTTC 420
QY 421 ATCATTCGATTCGCTGCGGCTGCTGCTGATTAAGAGGATGACGAAGAGACTG 480
DB 421 ATCATTCGATTCGCTGCGGCTGCTGCTGATTAAGAGGATGACGAAGAGACTG 480

QY 481 AGTTTGTGCAAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATGCTTCAATPAGA 540
DB 481 AGTTTGTGCAAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATGCTTCAATPAGA 540
QY 541 GTTGTCTGCAAAAGCTCAGGTAATATTTTGGCAGTGCAGTCCAGAAAGTCCGT 600
DB 541 GTTGTCTGCAAAAGCTCAGGTAATATTTTGGCAGTGCAGTCCAGAAAGTCCGT 600
QY 601 TTCTTACAGATCTCCGATGATGTCGATGACCGAAGGAGGACATTTGAAATTTACTG 660
DB 601 TTCTTACAGATCTCCGATGATGTCGATGACCGAAGGAGGACATTTGAAATTTACTG 660
QY 661 GGTTCAGTGTGTTATGCTCAGCAGAAAGATTAATACAGCTTGGTACATAGATTTTGG 720
DB 661 GGTTCAGTGTGTTATGCTCAGCAGAAAGATTAATACAGCTTGGTACATAGATTTTGG 720
QY 721 GTTCTTATTTTGTGCTTCTGCTGATGTTGTTGCAAAAGATGCCAATAAGAGTTT 780
DB 721 GTTCTTATTTTGTGCTTCTGCTGATGTTGTTGCAAAAGATGCCAATAAGAGTTT 780
QY 781 TCTACATATGCAATGCTCTGCTGAGGACAAATTTACATTGACAATTTGGCTATGGA 840
DB 781 TCTACATATGCAATGCTCTGCTGAGGACAAATTTACATTGACAATTTGGCTATGGA 840
QY 841 GACAAACTCCCTTAAGTGTGCGGAAAGATTTGCTTCTGCAAGCTTGTGCACTCTTGGC 900
DB 841 GACAAACTCCCTTAAGTGTGCGGAAAGATTTGCTTCTGCAAGCTTGTGCACTCTTGGC 900
QY 901 ATTTCTTTCTTTGCTTCTGCTGCGGCAATTTGCTGCTGCTGCTTGTGCAATTTGCA 960
DB 901 ATTTCTTTCTTTGCTTCTGCTGCGGCAATTTGCTGCTGCTGCTTGTGCAATTTGCA 960
QY 961 GAACAAACCCGCGCAAAACACTTTGAGAAAAGAAAGAAACCCAGCTGCCACCTCTTAC 1020
DB 961 GAACAAACCCGCGCAAAACACTTTGAGAAAAGAAAGAAACCCAGCTGCCACCTCTTAC 1020
QY 1021 TGTGTTTGGGCTAGTTCAGCAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAAGCA 1080
DB 1021 TGTGTTTGGGCTAGTTCAGCAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAAGCA 1080
QY 1081 CACTTGAAGCCTTTCACACCTGACGCTTACCA----- 1115
DB 1081 CACTTGAAGCCTTTCACACCTGACGCTTACCA----- 1115
QY 1116 --TCAGAGCTAAGTTTAAGAGAGCGAGTGGCTAGCCCGAGGCGCAGATTT 1173
DB 1116 --TCAGAGCTAAGTTTAAGAGAGCGAGTGGCTAGCCCGAGGCGCAGATTT 1173
QY 1174 AAGAGCGAAGCCTGATAGTGAAGAGAGTCCCAACGACGACATACAGCCGAG 1233
DB 1174 AAGAGCGAAGCCTGATAGTGAAGAGAGTCCCAACGACGACATACAGCCGAG 1233
QY 1201 AAGAGCGAAGCCTGATAGTGAAGAGAGTCCCAACGACGACATACAGCCGAG 1260
DB 1201 AAGAGCGAAGCCTGATAGTGAAGAGAGTCCCAACGACGACATACAGCCGAG 1260
QY 1234 GGCAGTCCCAAAAGTGCAGAGAGCTGAGCTTCAACGACGACGACGCTTCCGCGCC 1293
DB 1234 GGCAGTCCCAAAAGTGCAGAGAGCTGAGCTTCAACGACGACGACGCTTCCGCGCC 1293
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DB 1261 GGCAGTCCCAAAAGTGCAGAGAGCTGAGCTTCAACGACGACGACGCTTCCGCGCC 1320
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DB 1294 TGGCTGGGCTCAAAAGTGTCTACCCCAAAACGATATAGTGTGACACAGCCCTTGGC 1353
QY 1321 TGGCTGGGCTCAAAAGTGTCTACCCCAAAACGATATAGTGTGACACAGCCCTTGGC 1380
DB 1321 TGGCTGGGCTCAAAAGTGTCTACCCCAAAACGATATAGTGTGACACAGCCCTTGGC 1380
QY 1354 ACTGATGATGATATGATGAAAAAGATGCGAGTGTATGATAGTGAAGACCTCAC 1413
DB 1354 ACTGATGATGATATGATGAAAAAGATGCGAGTGTATGATAGTGAAGACCTCAC 1413
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DB 1381 ACTGATGATGATATGATGAAAAAGATGCGAGTGTATGATAGTGAAGACCTCAC 1440
QY 1414 CCACCACTTAAACTGTGATGAGCTATCAGATTTGAATTTCAATTTGCAAAACGG 1473
DB 1414 CCACCACTTAAACTGTGATGAGCTATCAGATTTGAATTTCAATTTGCAAAACGG 1473
QY 1441 CCACCACTTAAACTGTGATGAGCTATCAGATTTGAATTTCAATTTGCAAAACGG 1500
DB 1441 CCACCACTTAAACTGTGATGAGCTATCAGATTTGAATTTCAATTTGCAAAACGG 1500
QY 1474 AAGTTAAGAAACCTTACCTCATATGATGATTAAGATGTCAATTAATTTGCT 1533
DB 1474 AAGTTAAGAAACCTTACCTCATATGATGATTAAGATGTCAATTAATTTGCT 1533
QY 1501 AAGTTAAGAAACCTTACCTCATATGATGATTAAGATGTCAATTAATTTGCT 1560
DB 1501 AAGTTAAGAAACCTTACCTCATATGATGATTAAGATGTCAATTAATTTGCT 1560
QY 1534 GGTCACTGTGACATGTTGTGTAATTAAGCTTCAACAGCTGTTGATCAATTTCTT 1593
DB 1534 GGTCACTGTGACATGTTGTGTAATTAAGCTTCAACAGCTGTTGATCAATTTCTT 1593

Db 1561 GGTGATCTGGACATGTTGGTGTAGATTAAAGCCTTCACACGCTGTTGATCAATTTCTT 1620
1594 GGAAGAGGGCAATACATCATGATAGAGAGCCGAGAGAAATATACAGACGATGAG 1653
1621 GGAAGAGGGCAATACATCATGATAGAGAGCCGAGAGAAATATACAGACGATGAG 1680
1654 ACCACAGACATCTCATATATGCTGCTGGGTGGTCAAGTTGAAAAACAGTACAGTCC 1713
1681 ACCACAGACATCTCATATATGCTGCTGGGTGGTCAAGTTGAAAAACAGTACAGTCC 1740
1714 ATGAGAGCCAGCTGAGCTGCTACTAGATCTATCAACAGAGCTTCGGAAGAGCTCT 1773
1741 ATGAGAGCCAGCTGAGCTGCTACTAGATCTATCAACAGAGTCTTCGGAAGAGCTCT 1800
1774 GCGTCAGCCCTGCTTGGCTTCACTTCCAGATCCACCTTTTGAATGTGAACAGACATCT 1833
1801 GCGTCAGCCCTGCTTGGCTTCACTTCCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
1834 GAGATCAAGCCCTGCTGAGATGAGCAAGATCTTTCGGGTGGTCCGCAAAACAGTGGCTGC 1893
1861 GAGATCAAGCCCTGCTGAGATGAGCAAGATCTTTCGGGTGGTCCGCAAAACAGTGGCTGC 1920
1894 TTATCCAGATCACTAGTGGCAACATCTCGAGAGCCCTGAGTTCACTTTCGAGCCCAAT 1953
1921 TTATCCAGATCACTAGTGGCAACATCTCGAGAGCCCTGAGTTCACTTTCGAGCCCAAT 1980
1954 GAGTTCACTGCTGAGCTTCTACGCGCTTACGCTTACGCTTACGCTTACGCTTACGCT 2013
1981 GAGTTCACTGCTGAGCTTCTACGCGCTTACGCTTACGCTTACGCTTACGCTTACGCT 2040
2014 GTGCGCATTTGTTCAAGCGATGCTGAGCAGTGGCAGCCACCAACCATTTGCAACCA 2073
2041 GTGCGCATTTGTTCAAGCGATGCTGAGCAGTGGCAGCCACCAACCATTTGCAACCA 2100
2074 ATTAATTCAGGACCCCAAGCCAGCAGCCCAACCACTTTACAGATCCCACTTCCTCCCA 2133
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2134 GCGATCAAGCATCTGCGCCAGCCAGAAACTGTGACACCTTAACCTTCGAGGCTTACAGAA 2193
2161 GCGATCAAGCATCTGCGCCAGCCAGAAACTGTGACACCTTAACCTTCGAGGCTTACAGAA 2220
2194 AGCATTTCTGACGTCACACCTGCTTGTGCTGCTGCAAGAAATGTTCAAGTTCGACAG 2253
2221 AGCATTTCTGACGTCACACCTGCTTGTGCTGCTGCAAGAAATGTTCAAGTTCGACAG 2280
2254 TCAATTCACCAAGGACCGTTCTATGAGAAAGCTTTGACATGGAAGAGAAACTCTG 2313
2281 TCAATTCACCAAGGACCGTTCTATGAGAAAGCTTTGACATGGAAGAGAAACTCTG 2340
2314 TTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2373
2341 TTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
2374 ATGAGTTCGACGTCAGGAACTATATACACTTTGAGGAGTGAATGAGTTCGCTCAGA 2433
2401 ATGAGTTCGACGTCAGGAACTATATACACTTTGAGGAGTGAATGAGTTCGCTCAGA 2460
2434 GCGACCAAGATTTTAAACCCAAATGAGGAGATTCAAATTTGTTATTAACATGATGAAG 2493
2461 GCGACCAAGATTTTAAACCCAAATGAGGAGATTCAAATTTGTTATTAACATGATGAAG 2520
2494 GTGGGTCGCGAGAGACAGACAGACACTTTGATGCGGACCGGAGCTGCTCCAGGAA 2553
2521 GTGGGTCGCGAGAGACAGACAGACACTTTGATGCGGACCGGAGCTGCTCCAGGAA 2580
2554 GCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2613
2581 GCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
2614 AAGCAGAGAGAAAGTACAGATGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2667

Db 2641 AAGCAGAGAGAAAGTACAGATGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2694
RESULT 5
US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeeila, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNO5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; NAME/KEY: CDS
; LOCATION: (10)..(2703)
; OTHER INFORMATION: KCNO5-1
US-09-810-796-1
Query Match 98.5%; Score 2626.4; DB 10; Length 3071;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;
Db 1 ATGAAGATGTGAGTGGGCGCGGAGGAGTGTCTGTAATCTGCGCAGCCGCAAGGGC 60
10 ATGAAGATGTGAGTGGGCGCGGAGGAGTGTCTGTAATCTGCGCAGCCGCAAGGGC 69
QY 61 GAGGCGCTGTACTGCTGGGACACCGCGGCGCAAGCTTGGTGGCGGCGGCGGCTG 120
DB 70 GAGGCGCTGTACTGCTGGGACACCGCGGCGCAAGCTTGGTGGCGGCGGCGGCTG 129
QY 121 AGGAGAGCCCGCGGCGCAAGCAGGCGCGCGATGAGCCTGCTGGGAAACCGCTCT 180
DB 130 AGGAGAGCCCGCGGCGCAAGCAGGCGCGCGATGAGCCTGCTGGGAAACCGCTCT 189
QY 181 TACACGAGTACAGAGCTGCGCGCAAGCTCAAGTACCGCGGCGTACAGAACTACCTG 240
DB 190 TACACGAGTACAGAGCTGCGCGCAAGCTCAAGTACCGCGGCGTACAGAACTACCTG 249
QY 241 TACACGAGTACAGAGCTGCGCGCGGCGTGGCGTTCATCTACAGCGTTGTTTCTG 300
DB 250 TACACGAGTACAGAGCTGCGCGCGGCGTGGCGTTCATCTACAGCGTTGTTTCTG 309
QY 301 CTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 310 CTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 369
QY 361 GCGTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 370 GCGTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429
QY 421 ATGATTCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 430 ATGATTCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 489
QY 481 AGGTTTCTGCAAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 490 AGGTTTCTGCAAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
QY 541 GTTGTCTTCTGCAAGAACTCAAGGTAATATTTTGGCAGCTGCTGCACTGAGAAGTCCGT 600
DB 550 GTTGTCTTCTGCAAGAACTCAAGGTAATATTTTGGCAGCTGCTGCACTGAGAAGTCCGT 609

QY 601 TTCCACAGATCCCGCATGCTGGCATGACCGAAGGGAGGACATTGGAATTAATCTG 660
DB 610 TTCCACAGATCCCGCATGCTGGCATGACCGAAGGGAGGACATTGGAATTAATCTG 669
QY 661 GGTTCAGTGTGTATGCTACAGCAAGGAATTAATCAGACTTGTATAGATTTTGG 720
DB 670 GGTTCAGTGTGTATGCTACAGCAAGGAATTAATCAGACTTGTATAGATTTTGG 729
QY 721 GTCTATTTTGTGCTCTTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 730 GTCTATTTTGTGCTCTTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789
QY 781 TCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 790 TCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849
QY 841 GACAAACCTCCCTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 850 GACAAACCTCCCTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
QY 901 ATTCTTTCTTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 910 ATTCTTTCTTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
QY 961 GAACAAACCCGCGAAGAACCTTTGAGAAAGAGAAACCCGAGCTCCAACTTCTAG 1020
DB 970 GAACAAACCCGCGAAGAACCTTTGAGAAAGAGAAACCCGAGCTCCAACTTCTAG 1029
QY 1021 TGTGTTGGCGTATGTCAGCAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAGCA 1080
DB 1030 TGTGTTGGCGTATGTCAGCAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAGCA 1089
QY 1081 CACTGGAAGGCTTGCACACCTGCGACCTTACCA----- 1115
DB 1090 CACTGGAAGGCTTGCACACCTGCGACCTTACCAAGAAAGAAACCAAGGGAAGCATCAAGC 1149
QY 1116 --TCAGAAAGCTAAGTTTAAAGAGCGAGTGCATGCTAGGCCCGAGGGGAGAGTATT 1173
DB 1150 AGTCAGAAAGCTAAGTTTAAAGAGCGAGTGCATGCTAGGCCCGAGGGGAGAGTATT 1209
QY 1174 AAGAGCGGACAAAGCTCTAGTACAGAGAGGTCCTCCAGCAAGCATCAAGCGCGAG 1233
DB 1210 AAGAGCGGACAAAGCTCTAGTACAGAGAGGTCCTCCAGCAAGCATCAAGCGCGAG 1269
QY 1234 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAACGACGGAACCGGCTTCGGGCC 1293
DB 1270 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAACGACGGAACCGGCTTCGGGCC 1329
QY 1294 TCGCTGCGCTCAAAAGTTTTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGGC 1353
DB 1330 TCGCTGCGCTCAAAAGTTTTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGGC 1389
QY 1354 AACTGATATGATATGATGAGAAAGAGATGCCAGTGTATGATGATGAGAAAGCTCACC 1413
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DB 1450 CCACACCTTAAACCTGATTCAGAGCTATCAGAAATTAATGAAATTTTCAATGCAAAAGG 1509
QY 1474 AAGTTTAAAGAAAGCTTACGTCATATGATGATGATGATGATGATGATGATGATGAT 1533
DB 1510 AAGTTTAAAGAAAGCTTACGTCATATGATGATGATGATGATGATGATGATGATGAT 1569
QY 1534 GGTGATCTGAGCATGTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1593
DB 1570 GGTGATCTGAGCATGTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1629
QY 1594 GGAAGAGGCAATACATCATCATGATAGAGAGCGGAGAGAAATTAACGCAACATGAG 1653
DB 1630 GGAAGAGGCAATACATCATCATGATAGAGAGCGGAGAGAAATTAACGCAACATGAG 1689

QY 1654 ACCACAGCATCTCAGTATGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1713
DB 1690 ACCACAGCATCTCAGTATGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1749
QY 1714 ATAGAGTCCAAAGCTGAGTCTGCTACTAGACATCTATCAACAGAGTCTTGGAAAGCTCT 1773
DB 1750 ATAGAGTCCAAAGCTGAGTCTGCTACTAGACATCTATCAACAGAGTCTTGGAAAGCTCT 1809
QY 1774 GCTTCAGGCTCTGCTTGGCTTCAATCCAGATCCACCTTTTGAATGTGACAGCATCT 1833
DB 1810 GCTTCAGGCTCTGCTTGGCTTCAATCCAGATCCACCTTTTGAATGTGACAGCATCT 1869
QY 1834 GACTATCAAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1893
DB 1870 GACTATCAAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1929
QY 1894 TTATCCAGATCACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1953
DB 1930 TTATCCAGATCACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1989
QY 1954 GACTTCAGGCTCTGCTTGGCTTCAATCCAGATCCACCTTTTGAATGTGACAGCATCT 2013
DB 1990 GACTTCAGGCTCTGCTTGGCTTCAATCCAGATCCACCTTTTGAATGTGACAGCATCT 2049
QY 2014 GTGCCAAATTAATCAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2073
DB 2050 GTGCCAAATTAATCAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2109
QY 2074 ATAAATACGGGACCCCAAGGACGAGGACCCCAACCTTTACAGATCCACCTTCTCCCA 2133
DB 2110 ATAAATACGGGACCCCAAGGACGAGGACCCCAACCTTTACAGATCCACCTTCTCCCA 2169
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DB 2170 GGCATCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2229
QY 2194 AGCATTTCTGACGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2253
DB 2230 AGCATTTCTGACGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2289
QY 2254 TCAATATCTACCAAGAACCTGTTATGAGGAAAGCTTTGACATGGAAGGAACTCTG 2313
DB 2290 TCAATATCTACCAAGAACCTGTTATGAGGAAAGCTTTGACATGGAAGGAACTCTG 2349
QY 2314 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2373
DB 2350 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2409
QY 2374 ATCAGTTCGACCGAGAACTGATATACACTTTCAGGAGTGAAGTGAAGTGCACAGA 2433
DB 2410 ATCAGTTCGACCGAGAACTGATATACACTTTCAGGAGTGAAGTGAAGTGCACAGA 2469
QY 2434 GGCAGCCCAAGATTTTACCCCAATGAGGGAATCCAAATTTTATTAATGATGAGAG 2493
DB 2470 GGCAGCCCAAGATTTTACCCCAATGAGGGAATCCAAATTTTATTAATGATGAGAG 2529
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DB 2590 GCTGCTTTTGCATCAGACTCTTAAGGACTGGAAGGTTCAGATCATCTCAGAGATTTGT 2649
QY 2614 AAGGAGGAGAAAGTACAGATGCTTCAAGCTTGCCTCATGTCAAACTGAATTA 2667
DB 2650 AAGGAGGAGAAAGTACAGATGCTTCAAGCTTGCCTCATGTCAAACTGAATTA 2703

RESULT 6
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. US20020076809A1


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GENERAL INFORMATION:
APPLICANT: STEINMEYER, Klaus
APPLICANT: LERCHE, Christian
APPLICANT: SCHERER, Constanze
APPLICANT: SEEBOHM, Guiscard
APPLICANT: BOSCH, Andreas E.
TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCND5, A NEW TARGET FOR DISEASES OF CER
TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
FILE REFERENCE: 38005-119
CURRENT APPLICATION NUMBER: US/09/813,148
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: DE 100 13 732.6
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/194,041
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Homo sapiens
US-09-813-148-1

Query Match      98.1%  Score 2617.2  DB 10:  Length 3074:
Best Local Similarity 98.7%  Pred. No. 0:
Matches 2659:  Conservative  0:  Mismatches  8:  Indels  27:  Gaps  1:

OY  1  ATGAAGAGATGAGATCGGGCGGGGCGAGAGGTCGTCGTAACCTCGGACGCCAGGGGC 60
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DB  215  ATGAAGAGATGAGATCGGGCGGGGCGAGAGGTCGTCGTAACCTCGGACGCCAGGGGC 274
OY  61  GACGGCGTCTACTCTCTGGGCAACCGCGCGGCGCAGCGTTGGTGGCGCGGGTGGCCCTG 120
    |||||||
DB  275  GACGGCGTCTACTCTCTGGGCAACCGCGCGGCGCAGCGTTGGTGGCGCGGGTGGCCCTG 334
OY  121  AGGAGAGCGCGCGGGGCGAGAGGAGGCGCGGATGAGCGCTGCGGGAAGCGCTCTCT 180
    |||||||
DB  335  AGGAGAGCGCGCGGGGCGAGAGGAGGCGCGGATGAGCGCTGCGGGAAGCGCGCTCTCT 394
OY  181  TACACAGTAGCCAGAGCTGCCGCGCAACGTCAGTACCGCGGGGTGCAGACTACCTG 240
    |||||||
DB  395  TACACAGTAGCCAGAGCTGCCGCGCAACGTCAGTACCGCGGGGTGCAGACTACCTG 454
OY  241  TACACAGTCTGAGAGACCGCGCGGTGGCGCTTCACTACACAGCTTTCGTTTTCTC 300
    |||||||
DB  455  TACACAGTCTGAGAGACCGCGCGGTGGCGCTTCACTACACAGCTTTCGTTTTCTC 514
OY  301  CTGTCTTTGGTGTGATTTGTAGTCTTGTCTTACATCCCTGACACAAATTG 360
    |||||||
DB  515  CTGTCTTTGGTGTGATTTGTAGTCTTGTCTTACATCCCTGACACAAATTG 574
OY  361  GCCCTCAAGTTCCTTGTGATTCCTGAGTCTGATGATGATGCTGCTTGGTTGAGATTC 420
    |||||||
DB  575  GCCCTCAAGTTCCTTGTGATTCCTGAGTCTGATGATGATGCTGCTTGGTTGAGATTC 634
OY  421  ATCATTCGAATCTGCTGCGGGTGTGCTGTTGTCATATAGAGATGGCAAGAACTG 480
    |||||||
DB  635  ATCATTCGAATCTGCTGCGGGTGTGCTGTTGTCATATAGAGATGGCAAGAACTG 694
OY  481  AGGTTGCTGGAAGACCTTCTGTTTATATATACCATTTGTTTATGCGTTCAATAGCA 540
    |||||||
DB  695  AGGTTGCTGGAAGACCTTCTGTTTATATATACCATTTGTTTATGCGTTCAATAGCA 754
OY  541  GTTGTTCGCAAAAACACTCAGGTAATATTTTGGCACGTGCACTAGAACTCCGT 600
    |||||||
DB  755  GTTGTTCGCAAAAACACTCAGGTAATATTTTGGCACGTGCACTAGAACTCCGT 814
OY  601  TTCCTACAGATCTCTCGCATGGTGGCATGACCGAAGGGGAGGACCTGGAATTTACTG 660
    |||||||
DB  815  TTCCTACAGATCTCTCGCATGGTGGCATGACCGAAGGGGAGGACCTGGAATTTACTG 874
OY  661  GGTTCAGGTGTTATGTCACAGCAAGAAATATACAGCTTGGTACATAGGATTTTGG 720
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DB  875  GGTTCAGGTGTTATGCTCAGCAGCAAGAAATTAATCAAGCTTGTGACATAGATTTTGG 934
OY  721  GTTCTATATTTTTCGCTCTTCTGATCTGATGAGTGAAGAAAGATGCAATTAAGATTTT 780
    |||||||
DB  935  GTTCTATATTTTTCGCTCTTCTGATCTGATGAGTGAAGAAAGATGCAATTAAGATTTT 994
OY  781  TCTCATATGAGATGCTCTGCTGGGCGCAATTAATCATTTAGCACTATTTGCTATGGA 840
    |||||||
DB  995  TCTCATATGAGATGCTCTGCTGGGCGCAATTAATCATTTAGCACTATTTGCTATGGA 1054
OY  841  GACAAACTCCCTCACTTGGCTGGGAAGATTTGCTTTCGAGGCTTTGCACTCCTTGGC 900
    |||||||
DB  1055  GACAAACTCCCTCACTTGGCTGGGAAGATTTGCTTTCGAGGCTTTGCACTCCTTGGC 1114
OY  901  ATTCTTTCTTTGACCTTCCTGCGGCAATTCCTTGGCTCAGGTTTGCATTAAGATACAA 960
    |||||||
DB  1115  ATTCTTTCTTTGACCTTCCTGCGGCAATTCCTTGGCTCAGGTTTGCATTAAGATACAA 1174
OY  961  GAACAACACCGCCAGCAACACCTTTGAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAG 1020
    |||||||
DB  1175  GAACAACACCGCCAGCAACACCTTTGAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAG 1234
OY  1021  TGTGTTGGCGTGAATTAACGACCTGATGGAATGCTTTCCATTGCAACTGGAAGCCA 1080
    |||||||
DB  1235  TGTGTTGGCGTGAATTAACGACCTGATGGAATGCTTTCCATTGCAACTGGAAGCCA 1294
OY  1081  CACTTGAAGGCTTGCACACCTGCAACCTTACCA----- 1115
    |||||||
DB  1295  CACTTGAAGGCTTGCACACCTGCAACCTTACCAAGAAAGAAAGAAAGAAAGAAAGAAAG 1354
OY  1116  --TCAGACGTAAGTTTAAAGAGGAGTGGCGATGGTAGGCCCGAGGGCGAGATATT 1173
    |||||||
DB  1355  AGTCAGACGTAAGTTTAAAGAGGAGTGGCGATGGTAGGCCCGAGGGCGAGATATT 1414
OY  1174  AACAGCGGACAAACCTCAGTAGTGAAGAGGTCCCAAGCACCGACATCACAGCCGAG 1233
    |||||||
DB  1415  AAGAGCGGACAAACCTCAGTAGTGAAGAGGTCCCAAGCACCGACATCACAGCCGAG 1474
OY  1234  GGCAGTCCCAACCAAGTGAAGAGAGTGGAGCTTCAAGACCGAAGCCGCTTCCGCGCC 1293
    |||||||
DB  1475  GGCAGTCCCAACCAAGTGAAGAGAGTGGAGCTTCAAGACCGAAGCCGCTTCCGCGCC 1594
OY  1294  TCGGTGGCGCTCAAAAGTCTCAGCCCAAAACCAAGTATAGTGTGAACAGCCCTTGGC 1353
    |||||||
DB  1535  TCGGTGGCGCTCAAAAGTCTCAGCCCAAAACCAAGTATAGTGTGAACAGCCCTTGGC 1594
OY  1354  ACTGATGATGATATGATGAAGAAAGATGCCAGTGTGATGATGATGATGATGATGATGAT 1413
    |||||||
DB  1595  ACTGATGATGATATGATGAAGAAAGATGCCAGTGTGATGATGATGATGATGATGATGAT 1654
OY  1414  CCACACCTTAAACCTGATCGAGATCGAGATTCAGAAATTAATGAATTTCAATGTCGAAACGG 1473
    |||||||
DB  1655  CCACACCTTAAACCTGATCGAGATTCAGAAATTAATGAATTTCAATGTCGAAACGG 1714
OY  1474  AAGTTTAAGAAAGCTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1533
    |||||||
DB  1715  AAGTTTAAGAAAGCTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1774
OY  1534  GGTCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1593
    |||||||
DB  1775  GGTCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1834
OY  1594  GGAAGAGGCAAAATACATCAGATTAAGAAAGAGCGGAGAGAAATTAACAGCAGACATGAG 1653
    |||||||
DB  1835  GGAAGAGGCAAAATACATCAGATTAAGAAAGAGCGGAGAGAAATTAACAGCAGACATGAG 1894
OY  1654  ACCACAGAGATCTAGATGCTGCTGCTGCGGAGGAGCAAGTGAAGAAAGAGTACAGTCC 1713
    |||||||
DB  1895  ACCACAGAGATCTAGATGCTGCTGCTGCGGAGGAGCAAGTGAAGAAAGAGTACAGTCC 1954
OY  1714  ATAGAGTCCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1773
    |||||||
DB  1955  ATAGAGTCCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2014
    |||||||

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QY 1774 GCGTCAGCCCTGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGACAGACATCT 1833
 Db 2015 GCGTCAGCCCTGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGACAGACATCT 2074
 QY 1834 GACTTCAAAAGCCCTGTGGATAGCAAAAGATCTTGGGTTCGCGCAAAAGAGTGGCTGC 1893
 Db 2075 GACTTCAAAAGCCCTGTGGATAGCAAAAGATCTTGGGTTCGCGCAAAAGAGTGGCTGC 2134
 QY 1894 TTATCCAGATCACTAGTGGCCCACTTCGAGAGGCGTGCATTTATTTGAGCCCAAT 1953
 Db 2135 TTATCCAGATCACTAGTGGCCCACTTCGAGAGGCGTGCATTTATTTGAGCCCAAT 2194
 QY 1954 GAGTTCACTGCGCCAGACTTTTACGCGCTTACGCTTATGACAGTCAACCAACAG 2013
 Db 2195 GAGTTCACTGCGCCAGACTTTTACGCGCTTACGCTTATGACAGTCAACCAACAG 2254
 QY 2014 GTGCAATTTAGTCAAAAGGATGGCTGACAGATGGCAGCCCAACCACTTGCACCA 2073
 Db 2255 GTGCAATTTAGTCAAAAGGATGGCTGACAGATGGCAGCCCAACCACTTGCACCA 2314
 QY 2074 ATAAATACGGCACCACAGCCAGCAGCCCACTTACAGATCCCACTTCTCTCCCA 2133
 Db 2315 ATAAATACGGCACCACAGCCAGCAGCCCACTTACAGATCCCACTTCTCTCCCA 2374
 QY 2134 GGCATCAAGATCTGCGCCAGCCAGCAAACTTGCACCCCTAACCCTGACAGCTTACAGAA 2193
 Db 2375 GGCATCAAGATCTGCGCCAGCCAGCAAACTTGCACCCCTAACCCTGACAGCTTACAGAA 2434
 QY 2194 AGCATTTCTAGCTCAACCACTGCTTGTGCTTCCCAAGAAATTTGTCAGCTTGCACAG 2253
 Db 2435 AGCATTTCTAGCTCAACCACTGCTTGTGCTTCCCAAGAAATTTGTCAGCTTGCACAG 2494
 QY 2254 TCAAAATCTCAACCAAGACCGCTTATAGAGAAAGCTTTGACATGGAGAGAGAACTCTG 2313
 Db 2495 TCAAAATCTCAACCAAGACCGCTTATAGAGAAAGCTTTGACATGGAGAGAGAACTCTG 2554
 QY 2314 TTGTCTGTCTGCCATGGTGGCGAAGACTTGGGCAATCTTGTGCTGTGCAAACTCTG 2373
 Db 2555 TTGTCTGTCTGCCATGGTGGCGAAGACTTGGGCAATCTTGTGCTGTGCAAACTCTG 2614
 QY 2374 ATCAGGTGACCGAGAGACTGAAATATACAACTTTCAGGAGTGTCAAGTGGCTCCAGA 2433
 Db 2615 ATCAGGTGACCGAGAGACTGAAATATACAACTTTCAGGAGTGTCAAGTGGCTCCAGA 2674
 QY 2434 GGCAGCCCAAGATTTTACCCCAATGGAGGAGATCCCAATTTGTTTAACTGATGAAGAG 2493
 Db 2675 GGCAGCCCAAGATTTTACCCCAATGGAGGAGATCCCAATTTGTTTAACTGATGAAGAG 2734
 QY 2494 GTGGTCCCGAAGAGACAGACACTTTTATGCGCGCAGCCGAGCTGCCAGGGGA 2553
 Db 2735 GTGGTCCCGAAGAGACAGACACTTTTATGCGCGCAGCCGAGCTGCCAGGGGA 2794
 QY 2554 GCTGCTTGTGATGAGATCTCTAAGACTGGAAGTCAAGTCACTGACAGACTTTGT 2613
 Db 2795 GCTGCTTGTGATGAGATCTCTAAGACTGGAAGTCAAGTCACTGACAGACTTTGT 2854
 QY 2614 AAGCAGAGAGAAAGTACAGATGCGCTTGGCTTCAATCAAACTGAATTA 2667
 Db 2855 AAGCAGAGAGAAAGTACAGATGCGCTTGGCTTCAATCAAACTGAATTA 2908

; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KNOX POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DCS6ADLV
 ; CURRENT APPLICATION NUMBER: US/10/128,870
 ; CURRENT FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 09/105,058
 ; PRIOR FILING DATE: June 26, 1998
 ; PRIOR APPLICATION NUMBER: 60/055,599
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 2169
 ; TYPE: DNA
 ; ORGANISM: MOUSE
 ; US-10-128-870-22

Query Match 17.8%; Score 475.6; DB 9; Length 2169;
 Best Local Similarity 57.0%; Pred. No. 6.7e-130;
 Matches 1022; Conservative 0; Mismatches 664; Indels 108; Gaps 4;

QY 64 GGCCTGTACTGTGGGCGACCCGGGCGCCAGCTTGTGGCGGCGGCGTGGAG 123
 Db 67 GGCCTGTGGGCGTGGACCCCGGCGCGCCGACTCCACACCGCAGCGGCTACTCATC 126
 QY 124 GAGAGCCGCGGGGCAAGCAGGGGCGCGATGAGCTGTGGGGAAGCGCTCTTAC 183
 Db 127 GCGGGCTCCGAGGCGCCCAAGCGCGGACGCTTTGAGCAAGCCGCGGACGGGCGG 186
 QY 184 ACGATGAGCCAGAGCTCCGCGGCAAGCTACAGTACCGCGGGGTGCAAACTACTATAC 243
 Db 187 GAGGCGGGAAGCCCGCGAAGCGCAAGCTTACCGCAAGCTGAGAAATTCCTCTAC 246
 QY 244 AAGTGTGAGAGACCCCGCGGCTGGCGTTCATCAGCAGCTTTCGTTTCTCTCT 303
 Db 247 AAGTGTGAGAGCGCGCGCGCGCTGGGCTTCATCAGCAGCTTTCGTTTCTCTCT 306
 QY 304 GTCCTTGTGCTGATTTTGTGATGTTTCTACATCCCTGAGCAACAAATTTGCC 363
 Db 307 GTCCTTGTGCTGATTTTGTGATGTTTCTACATCCCTGAGCAACAAATTTGCC 366
 QY 364 TCAAGTTCCTTGTGATTCCTGAGTTCGATGATGATGATGATGATGATGATGATGAT 423
 Db 367 GAGGGGGCCCTTACATCTTGAATCGTACATCTGATGATGATGATGATGATGATGAT 426
 QY 424 ATTGCAATGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
 Db 427 GTGAGGATCTGGGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
 QY 484 TTTGCTGAAAGCCCTTGTGATTCCTGAGTTCGATGATGATGATGATGATGATGATGAT 543
 Db 487 TTTGCTGAAAGCCCTTGTGATTCCTGAGTTCGATGATGATGATGATGATGATGATGAT 546
 QY 544 GTTTCGAAAACTCAGAGTAATTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
 Db 547 CTGGCTGTGGTTCCCAAGGCAATGTCTTGGCACATCTTGGGCTTGGGAGCTTGGG 606
 QY 604 CTACAGATCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
 Db 607 TTTGCAATCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
 QY 664 TCAAGTGTGATGCTCAGCAGCAAGAAATTAATCAAGTGTGATGATGATGATGATGAT 723
 Db 667 TCGGTAGTCTACGCTCAGCAGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
 QY 724 CTATTTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
 Db 727 CTATTTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
 QY 784 ACATATGACATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 Db 787 ACATATGACATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846

RESULT 7
 US-10-128-870-22
 ; Sequence 22, Application US/10128870
 ; Patent No. US20020168724A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blau, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Gribokoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.

844 AAACCTCCCTACTTGGCTGGAGATTGCTTTCGACGCTTTCACCTCTTGGCAT 903
847 AAGTACCTCAGACCTGGAGCGGAGGCTGCGACGACCTTACCTCATTTGGTCTC 906
904 TCTTTCTTGGCACTTCTCGCGGCAATCTTGGCTGAGTTTGGCAATTAAGTACAGAA 963
907 TCGTCTTCTTGGCTTCTCGCGGCAATTTGGGATTCGCGCTTGGCTTGAAGTCCAGAG 966
964 CAACACCGCCAAACACTTGTGAGAAAGAGAACCCAGCTGCGCACTTCACTTCACTGT 1023
967 CAGCATTCGGCAAAACACTTGTGAGAAAGCGGAGACCTTGGCGGAGTGTGATCCAGTCT 1026
1024 GTTTGGCTAGTCTTACCGACCTGATGAGAAATCTGTTTCACTTGCACCTTGAAGCCACAC 1083
1027 GCGTGAAGATTCATCTACTTAACCTTCACGACCGACCTGACCTCCACGTGAGTAC 1086
1084 T----- 1084
1087 TAGAGGGAGCACTGCTGCTCCCATGTACAGACTATCCACCTTGAACGACGCTGAG 1146
1085 -----TGAAGGCTTGCACACCTGC 1104
1147 CTGCTGAGGATCTCAAGACCAATCTGACCTTCAAGAAAGGACGACGACGAG 1206
1105 AGCCTTACCAATCAGAACTTAAGTAAAGGAGGAG---TGGCATGAGCTAGCCGAGG 1161
1207 CCATTCACCAAGTGAAGAGTTCAGTTGAAAGATCTGCTTCTTCCACCCCGGAGGATG 1266
1162 GGGCAGAGTATTAAGACCCGACCAAGCTCAGTATGATGACGAGGAGTCCGCAAGCAGC 1221
1267 GCTGCCAAGGAAAGGAGTCTCCCGACGACGAGCGTCCGCGGAGTCCCGACGCTGAT 1326
1222 ATCAGACCGGAGGCACTCCACCAAGTGCAGAGAGCTTGAAGCTTCAACGACGACGAG 1281
1327 CAGAGCTTATGACAGCCGAGAGAGTGCAGGAGCTGAGAGCTTGGTGAAGCCGAGC 1386
1282 CGCTTCGGGCGCTGCTGCGGCTCAAAAGTTCTCAGCCAAACAGATGATGATGATGAT 1341
1387 CGCAGACGAGGCTTTCGCGATTAAGGAGTCTCATTCGCGGAGAAATTCAGAAAGCAAG 1446
1342 ACAGCCCTTGCACCTGATGATATATGATGAGAAAGAGGAGGAGCTGATGATGATGAT 1401
1447 C---TCCCTGGGAGAGCATGCTGAGAGACAAAGAGCTTAACTGCGAGTCTTGTGACT 1503
1402 GAGACCTACCCACCACTTAAGTGTCAATGAGCTATCAGATTAAGTAAATTTAT 1461
1504 GAAATCTTACCTGCGCTCAAAAGTGAAGTGAAGAGCTGTGTGTATGCGGTTCTTG 1563
1462 GTTCAAAACGAGATTAAGAAAGCTTACGTCATGATGATGATGATGATGATGATGAT 1521
1564 GTATCTAAGCAAAAGTCAAGAGAGTGTGCGCATATGATGATGATGATGATGATGAT 1623
1522 CAATATCTGCTGCTCATCTGAGCATGTTGTGTAGATTTAAAGCTTCAAAACAGTGT 1581
1624 CAGTACTGCGTGAACACTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1683
1592 GATCAAAATTTTGGAAAGGCAAAATTCATGATGATGATGATGATGATGATGATGAT 1641
1684 GACCAAGATTTGGGCGGAGGCGCCAAACATTAAGGATTAAGGAG---TCGCAACCAAGGCCA 1740
1741 GCGGAAACGAGAGCTGCCGAAAGAGCCCAAGCATGATGAGGAGGCTTGGGAAAGTGGGAAA 1800
1702 CAGGTACAGTTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1755
1801 CAGGTCTGCTGCTGATGAGAAAGAGCTGAGCTTGTGATGATGATGATGATGATGAT 1854

RESULT 8
US-10-128-870-1
; Sequence 1, Application US/10128870
; Patent No. US20020168724A1

GENERAL INFORMATION:
APPLICANT: Blumar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neuberger, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KNOX POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: DC584dV
CURRENT APPLICATION NUMBER: US/10/128,870
PRIORITY FILING DATE: 2002-04-24
PRIORITY FILING DATE: 09/10/05, 058
PRIORITY FILING DATE: June 26, 1998
PRIORITY FILING DATE: 60/055,599
PRIORITY FILING DATE: August 12, 1997
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 896
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
FEATURE:
OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
US-10-128-870-1
Query Match 17.5%; Score 465.4; DB: 9; Length 896;
Best Local Similarity 53.7%; Pred. No. 3.6e-127;
Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;
DB 190 AGCAGAGCTCCCGGCAAGCTGACGAGTACCGGCGGAGGAGCAACTTACAGCTG 249
DB 13 RGSMSCCMSYSAAGMGAACGCCWSTACCGSMRSMSCARMTTMTCTACAGCYS 72
DB 250 CTGAGAGACCCCGCGGCTGGGCGTTTCATACCAAGCTTTCGTTTTCCTGTTCTTT 309
DB 73 CTGAGAGACCCCGCGGCTGGGCGTTTCATACCAAGCTTTCGTTTTCCTGTTTCTTT 132
DB 310 GATTGCTGATTTTGTGAGTGTGTTTTCATCCATCCCTGAGGACACAAATTTGGCCCAAGT 369
DB 133 KSTCCYBTRKCTGCTGTS-YKWCACOMTCAAGAGTATGACAAAKRYTCBRRGRS 191
DB 370 TGCCCTTGATCTGAGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 429
DB 192 KSSCTTYMSWMTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 251
DB 430 ATCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 489
DB 252 ATCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
DB 490 GCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 549
DB 312 MCGAATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
DB 550 GCAAAACTCAGGATTAATTTTGGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 609
DB 372 GYBGHMMCCARGGCAAYTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
DB 610 ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669
DB 429 ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
DB 670 GTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 729
DB 489 KCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
DB 730 TTTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789
DB 549 CTCKCYCTRTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608


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11 RESULT 11
12 US-10-128-870-3
13
14 ; Sequence 3, Application US/10128870
15 ; Patent No. US20020168724A1
16 ;
17 ; GENERAL INFORMATION:
18 ;
19 ; APPLICANT: Blonar, Michael A.
20 ; APPLICANT: Dworetzky, Steven
21 ; APPLICANT: Grikoff, Valentin K.
22 ; APPLICANT: Levesque, Paul C.
23 ; APPLICANT: Little, Wayne A.
24 ; APPLICANT: Neubauer, Michael G.
25 ; APPLICANT: Yang, Wen-pin
26 ;
27 ; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
28 ;
29 ; FILE REFERENCE: DC58ADIY
30 ;
31 ; CURRENT APPLICATION NUMBER: US/10/128,870
32 ;
33 ; CURRENT FILING DATE: 2002-04-24
34 ;
35 ; PRIOR APPLICATION NUMBER: 09/105,058
36 ;
37 ; PRIOR FILING DATE: June 26, 1998
38 ;
39 ; PRIOR APPLICATION NUMBER: 60/055,599
40 ;
41 ; PRIOR FILING DATE: August 12, 1997
42 ;
43 ; NUMBER OF SEQ ID NOS: 28
44 ;
45 ; SOFTWARE: Patentln Ver. 2.1
46 ;
47 ; SEQ ID NO 3
48 ;
49 ; LENGTH: 900

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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: 900 nucleotides of human KCNQ2
OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-10-128-870-3

Query Match 15.8%; Score 421.4; DB 9; Length 900;
Best Local Similarity 68.6%; Pred. No. 3,7e-114;
Matches 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

194 AGAGCTGCGGCGCAACGTCACAGTACCGGGGTGACAGACTACCTTACAAAGTGGTGG 253
17 ACCCCCCCAAGCGCAACGCTTACCGCAAGCTGCAAGATTCCTACACAGCTGCTGG 76
254 AGAGACCGCGCGCGGCGGCTGACACAGCTTTCGTTTCTCTCTCTCTCTCTCTCT 313
77 AGCGGCGCGCGCGGCTGCGGCTTATATACACCGCTACGCTGCTCTCTCTCTCTCT 136
314 GCTTGAATTTGTCAGTGTTCATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 373
137 GCTTGAATTTGTCAGTGTTCATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 196
374 TCTTGAATTTGTCAGTGTTCATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 433
197 TCTTGAATTTGTCAGTGTTCATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 256
434 GCTTGAATTTGTCAGTGTTCATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 493
257 GCGGCGCGCGCGGCTGCGGCTTATATACACCGCTGCAAGATTCGAGAGGCGGCGCG 316
494 AGCGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 553
317 AACCGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 376
554 AACCGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 613
377 GCTTGAATTTGTCAGTGTTCATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 436
614 TCGGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 673
437 TCGGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 496
674 ATGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 733
497 ATGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 556
734 GCTTGAATTTGTCAGTGTTCATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 793
557 GCTTGAATTTGTCAGTGTTCATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 616
794 ATGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 853
617 ATGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 676
677 AGAGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 736
914 CAGTCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 913
737 CAGTCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 796
974 AGAAGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 1033
797 AGAAGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC 856
1034 GATAGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC
857 TTTAGCTTCTGTATATACATCCCTGACACACAAATTTGGCTTCAAGTTGCC

Sequence 5, Application US/10128870
Patent No. US2002016872A1
GENERAL INFORMATION:
APPLICANT: Blauar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: DC58ADIV
CURRENT FILING DATE: 2002-04-24
PRIOR FILING DATE: 09/105,058
PRIOR APPLICATION NUMBER: 60/055,599
PRIOR FILING DATE: August 12, 1997
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 900
TYPE: DNA
ORGANISM: MOUSE
FEATURE:
OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-10-128-870-5

Query Match 15.8%; Score 420.6; DB 9; Length 900;
Best Local Similarity 68.7%; Pred. No. 6.4e-114;
Matches 579; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

204 GCGCAGCTGCAAGTACCGGCGGCTGCAAGTACCGTACACAGTGGTGGAGAGCCCG 263
27 GCGCAGCTGCAAGTACCGGCGGCTGCAAGTACCGTACACAGTGGTGGAGAGCCCG 86
264 GCGCAGCTGCAAGTACCGGCGGCTGCAAGTACCGTACACAGTGGTGGAGAGCCCG 323
87 GCGCAGCTGCAAGTACCGGCGGCTGCAAGTACCGTACACAGTGGTGGAGAGCCCG 146
324 GCGCAGCTGCAAGTACCGGCGGCTGCAAGTACCGTACACAGTGGTGGAGAGCCCG 383
147 GCGCAGCTGCAAGTACCGGCGGCTGCAAGTACCGTACACAGTGGTGGAGAGCCCG 206
384 GCGCAGCTGCAAGTACCGGCGGCTGCAAGTACCGTACACAGTGGTGGAGAGCCCG 443
207 GCGCAGCTGCAAGTACCGGCGGCTGCAAGTACCGTACACAGTGGTGGAGAGCCCG 266
444 GCGCAGCTGCAAGTACCGGCGGCTGCAAGTACCGTACACAGTGGTGGAGAGCCCG 503
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624 GCGCAGCTGCAAGTACCGGCGGCTGCAAGTACCGTACACAGTGGTGGAGAGCCCG 683
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| Db | 132 | CTGGGGGGCTTGATTTCTGGGTGTCGACCAATTCAGAGATATGAGACTGCTCGGG | 191 | | |
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| | 111 | | | | |

```

1  APPLICANT:  Blanar, Michael A.
2  APPLICANT:  Dworetzky, Steven
3  APPLICANT:  Glibkoff, Valentin K.
4  APPLICANT:  Levesque, Paul C.
5  APPLICANT:  Little, Wayne A.
6  APPLICANT:  Neubauer, Michael G.
7  APPLICANT:  Yang, Wen-Pin
8  TITLE OF INVENTION:  KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
9  FILE REFERENCE:  DC58adiV
10 CURRENT APPLICATION NUMBER:  US/10/128, 870
11 CURRENT FILING DATE:  2002-04-24
12 PRIOR APPLICATION NUMBER:  09/105,058
13 PRIOR FILING DATE:  June 26, 1998
14 PRIOR APPLICATION NUMBER:  60/055,599
15 PRIOR FILING DATE:  August 12, 1997
16 NUMBER OF SEQ ID NOS: 28
17 SOFTWARE:  Patentin Ver. 2.1
18 SEQ ID NO 7
19 LENGTH: 735
20 TYPE:  DNA
21 ORGANISM:  RAT
22
23 US-10-128-870-7

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| Query Match | 12.5% | Score 334.2 | DB 9 | Length 735 |
| Best Local Similarity | 68.4% | Pred. No. 1.9e-88 | | |
| Matches 462: Conservative | 0 | Mismatches 213 | Indels 0 | Gaps 0 |


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QY 372 CCTCTGATCCCTGAGATTCGTGATGATTCGCTCTTTGGATTGATCATTCATGCAAT 431
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RESULT 15
US-09-840-125-1
; Sequence 1, Application US/09840125
; Patent No. US20020061524A1
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: Keating, Mark T.
; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
; FILE REFERENCE: 2323-155
; CURRENT APPLICATION NUMBER: US/09/840,125
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/634,920
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,488
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (1)..(2028)
US-09-840-125-1
Query Match 10.0%; Score 267.8; DB 10; Length 2028;
Best Local Similarity 59.5%; Pred. No. 1,7e-68;
Matches 499; Conservative 0; Mismatches 322; Indels 18; Gaps 2;

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Db 796 CTGTACATGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 855
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Db 856 GACGCGGTGAACAGTACAGCGCGGTGAGTTGCGCACTAGCAAGATGCGCTGCTG 915
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Db 916 GGGGTGTACAGTACACACATCGCTATGAGGAGCAAGTGGCCAGAGTGGTGGG 975
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 Job time : 108 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 11, 2003, 17:21:17 ; Search time 3948 Seconds
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Title: US-09-810-796-5
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Searched: 2054640 seqs, 14551402878 residues
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 4527.5 | 99.6 | 2694 | 6 AX322509 | AX322509 Sequence |
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| 6 | 4513.5 | 99.3 | 3074 | 6 AX253254 | AX253254 Sequence |
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| 9 | 4328.5 | 93.0 | 2832 | 9 AF263835 | AF263835 Homo sapi |
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| 15 | 1804.5 | 39.7 | 2613 | 10 AF490773 | AF490773 Mus muscu |
| 16 | 1797 | 39.5 | 7420 | 9 HSKCND2 | AF074247 Homo sapi |
| 17 | 1790 | 39.4 | 2565 | 6 AF074247 | AF074247 Homo sapi |
| 18 | 1790 | 39.4 | 3195 | 9 AF074247 | AF074247 Homo sapi |
| 19 | 1786.5 | 39.3 | 2827 | 10 AB000497 | AB000497 Mus muscu |
| 20 | 1783.5 | 39.2 | 2750 | 6 AX456861 | AX456861 Sequence |
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| 24 | 1761 | 38.7 | 2920 | 10 AB000495 | AB000495 Mus muscu |
| 25 | 1758.5 | 38.7 | 2935 | 10 AB000494 | AB000494 Mus muscu |
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| 28 | 1617 | 35.6 | 120846 | 9 AL365232 | AL365232 Human DNA |
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| 31 | 1587.5 | 34.9 | 2755 | 6 AF033347 | AF033347 Homo sapi |
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| 36 | 1547.5 | 34.0 | 2766 | 10 AF091247 | AF091247 Rattus no |
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| 39 | 1226.5 | 27.0 | 1182 | 6 E13516 | E13516 Human mRNA |
| 40 | 1226.5 | 27.0 | 1435 | 6 A94977 | A94977 Sequence 4 |
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RESULT 1

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DEFINITION Sequence 1 from Patent WO0175108.
ACCESSION AX268474
VERSION AX268474.1 GI:16541652
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Hu, Y., Kieke, J.A., Turner, A.C., Nehls, M.C., Friedrich, G.B.,
Zambowicz, B. and Sanders, A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 01/5108-A 1 11-OCT-2001;
Lexicon Genetics Incorporated (US)
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source 1.2772
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 715 a 700 c 713 g 644 t
ORIGIN
Alignment Scores:
Pred. No.: 1.97e-312 Length: 2772
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-810-796-5 (1-888) x AX268474 (1-2772)
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Db 106 ATGAAGAGATGTGGAGATCGGGCGGGGCGAGGGGTCTGCTCAACTCGGACGCCAGCGGCGC 165
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
Db 166 GACGGCGCTGCTACTGCTGGCACCGCGCGCGCCACGCTCGGTGGCGGGCGGTGGCTG 225
QY 41 ArgGluSerArgArgGlyGlyGlyGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 226 AGGAGAGAGCCCGGGGCGAGCGGGGCGCGGATGAGCTGTGGGAGACCGCTCTCT 285
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 286 TACACGAGTAGCCAGACCTCGCGCGCACCTCAAGTACCGCGGGGTGCAGAACTACTCTG 345
QY 81 TyrAsnValLeuGluArgProArgGlyTyrPalaPheLeuTyrHisAlaPheValPheLeu 100
Db 346 TACAACTGCTGGAGAGACCCCGCGGCTGAGCTTCATCTACACGCTTCGTTTCTC 405
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RESULT 2
AX268476 3111 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 3 from Patent WO0175108.
ACCESSION AX268476
VERSION AX268476.1 GI:16541653

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KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Hu, Y., Kieke, J. A., Turner, A. C., Nehls, M. C., Friedrich, G. B.,
Zambrowicz, B. and Sands, A. T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 0175108-A 3 11-OCT-2001.
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Alignment Scores:
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Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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 DEFINITION Sequence 1 from Patent WO0192526.
 ACCESSION AX322509
 VERSION AX322509.1 GI:18093555
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

[illegible]

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| O | y | | 321 | GluGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaAlaSerLeuLiegln | 340 |
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| D | b | | 1021 | TGGTTTGGCGAGTAGTACGACAGCTGATGAAATCTGTTCCATTTGCATCGAACCTGAAGCCA | 1080 |
| O | y | | 361 | HisLysValAlaLeuHisThrCysSerProThr----- | 371 |
| D | b | | 1081 | CATTGAGAGCCCTWGCACACCTCGACAGCCCTCACGAAGAACAAGGGAAGCATCAAGC | 1140 |
| O | y | | 372 | AsnGlnLysLeuSerPheLysGlnArgValArgMetAlaSerProArgGlyGlnSerLle | 391 |
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| D | b | | 1201 | AAGAGCCGACACCTCAGTAGGTGACAGAGAGTCCCCAAGACCCACATCATCAGACGGAG | 1260 |
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| O | y | | 492 | LysPheLysGlnThrLeuArgProTrpAspValLysAspValLleGlnGlnYrSerAla | 511 |
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| D | b | | 1621 | GGAAAAAGGCAAAATCCATCATGATGAAGAAGACCCAGAGAAATTAACAGCAGACATGAG | 1680 |
| O | y | | 552 | ThrThrAspAspLeuSerMetLeuGlnArgValValLysValGlnLysGlnValGlnSer | 571 |
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| D | b | | 1741 | ATAGAGTCCAAAGCGAGCTCCCTACTAGACATTTATCAACAGGTCCCTTGGCAAAAGCTCT | 1800 |
| O | y | | 592 | AlaSerAlaLeuAlaLeuAlaSerPheGlnLleArgProPheGlnLysGlnGlnThrSer | 611 |
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| Oy | 612 | AspyrrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnaspSerGlyCys | 631 |
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| Oy | 712 | AlaIleLysHisIleuproAlagProGluInthrLeuHisProasnProAlaGlyLeuGlnGlu | 731 |
| Db | 2161 | GCCATCAAGATCTGCCCCAGGCCCAAGAACTCTGCACCCCTAACCTCGAGGCTTACAGGA | 2220 |
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| Db | 2401 | ATCAGGTCGACCCGAGGAACGTGAATACACTTTTCAGGGAAGATGAGTCAAAGGCTCCAGA | 2460 |
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| DEFINITION | Sequence 1 from Patent WO0077035. | DNA | linear |
| ACCESSION | AX056817 | | PAT 17-JAN-2001 |
| VERSION | AX056817.1 | GI:12309758 | |
| KEYWORDS | | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| REFERENCE | Jentsch,T.J. | | |
| AUTHORS | Novel potassium channels and genes encoding these potassium | | |
| TITLE | channels | | |
| JOURNAL | Patent: WO 0077035-A 1 21-DEC-2000; | | |

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BASE COUNT 865 a 749 c 745 g 778 t

ORIGIN

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Score: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 9
Query Match: 99.57% Indels: 9
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US-09-810-796-5 (1-888) x AX056817 (1-3137)

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LOCUS AX253254
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ACCESSION AX253254
VERSION AX253254.1 GI:16073802
KEYWORDS
SOURCE human.
ORGANISM Homo Sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3074)
AUTHORS Lerche,C., Scherer,C., Seebom,G., Busch,A. and Steinmeyer,K.
TITLE potassium channel protein kno5, a target for diseases of central
nervous system and cardiovascular system
JOURNAL Patent: WO 01/0811-A 1 27-SEP-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
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| OY | 361 | HisLeuLysAlaLeuHisThrCysSerProThr----- | 371 |
| Db | 1295 | CACCTTGAAAGCCTTGACACCTGCACCCCTACCAAGAAAGAACAGGGAGCATCAAGC | 1354 |
| OY | 372 | AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle | 391 |
| Db | 1355 | ACTCGAAGACTAAGTTTAAAGGAGCGAGTGCGCATGGCTAGCCCAAGGGGCGAGAGATT | 1414 |
| OY | 392 | LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu | 411 |
| Db | 1415 | AAGAGCCGACAAAGCCTAGTAGGAGACAGGAGGTCGCCAAACGACGACATACAGCCGAG | 1474 |
| OY | 412 | GlySerProThrLysValGlnLysSerTyrSerPheAsnAspArgTyrArgPheArgPro | 431 |
| Db | 1475 | GGCAGTCCCAACAAAGTGCAGAGAGAGCTGGAGCTTCAACAGCCAGACCCGCTCCGGCC | 1534 |
| OY | 432 | SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly | 451 |
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| Db | 1595 | ACTGATGATGATATGATGAGAAAAGGATGCCAGTGATGATATGAGGAGAGACTCAC | 1654 |
| OY | 472 | ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg | 491 |
| Db | 1655 | CCACCACTTAAACTGTCATTCGAGCTATCAGAAATTATGAATTTTCATGTTGCCAAAACG | 1714 |
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| OY | 512 | GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu | 531 |
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| Db | 1835 | GGAAAAGGCCAAATCACATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAACATGAG | 1894 |
| OY | 552 | ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer | 571 |
| Db | 1895 | ACCACAGACGATCTCAGTATGCTGCTGGGTGTCAAAGTTTGAAAAACAGTACAGTCC | 1954 |
| OY | 572 | IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer | 591 |
| Db | 1955 | ATAGAATCCAAAGCTGAGCTGCTACTGACATCTATCAACAGGCTCTTGGAAAGGCTCT | 2014 |
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 LOCUS Sequence 5 from Patent WO232960.
 DEFINITION AX456864
 ACCESSION AX456864
 VERSION 1 GI:21715731
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Argentieri, T.M. and Sheldon, J.H.
 TITLE Methods of selecting compounds for modulation of bladder function
 JOURNAL Patent: WO 0232960-A 5 25-APR-2002;
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 Best Local Similarity: 98.66% Mismatches: 2
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BASE COUNT 788 a 784 c 789 g 713 t
ORIGIN
CRAGSTDLSPHVLK*

Alignment Scores:

Pred. No.: 5,41e-310 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
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US-09-810-796-5 (1-888) x AF249278 (1-3074)

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LOCUS Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,
partial cds.
AF263836
AF263836.1 GI:8132998

ACCESSION
VERSION AF263836.1 GI:8132998

KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 3108)
Kniazeva, M. and Han, M.
A new gene of the voltage-gated potassium channel KCNQ family,
KCNQ5, is a candidate gene for retinal disorders
Unpublished
2 (bases 1 to 3108)
Kniazeva, M. and Han, M.
Direct Submission
Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
Porter Biosciences Bldg., Boulder, CO 80309, USA
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US-09-810-796-5 (1-888) x AF263836 (1-3108)
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 REFERENCE
 AUTHORS Jentsch,T.J.
 TITLE Novel potassium channels and genes encoding these potassium
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US-09-810-796-5 (1-888) x AX032994 (1-2335)

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 REFERENCE 1
 AUTHORS Argentieri, T.M. and Sheldon, J.H.
 TITLE Methods of selecting compounds for modulation of bladder function
 JOURNAL Patent: WO 0232960-A 4 25-Apr-2002;
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| Db | 1462 | AATGCCACCACTCCCAAGACGAGACAGCTGGGTGAGGCGACACGCCCAACAGGTGCA | 1521 |
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| Qy | 438 | rGlnProLYsProVALLeAspALAspThraLALeugLYThrAspAspVALTyraSpGL | 458 |
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| Qy | 478 | EArGALALeArgILeMeCysPheHisVALALALysArGLysPheLYsGLuThrLeuAr | 498 |
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| Qy | 498 | qPOTyTrAspVALysAspVALLeGLuGlnTYrSerAlaGLYHisLeuSpmelleuCY | 518 |
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| Qy | 555 | PLAsuSerMeLeuGLYArgVALYALysVALGLuLYsGLInVALGlnSerILeGLuSerLY | 575 |
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| Qy | 575 | sLeuAspCysLeuLeuAspILeTYrGLInGLInVALLeuArgLYsLYsSerALAserAlALe | 595 |
| Db | 1978 | GCTGGACCTGCTGTGGCTTCATTTGCGCTGCTGCTCGCTGAGCACTTGCGC----- | 2032 |
| Qy | 595 | uAlALeUAlAserPheGLInILeProProPheGLYcysGLuGLInThraSerAsPYrGLInSe | 615 |
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| DEFINITION | Rattus norvegicus potassium channel (KCNO2) mRNA, complete cds. | | | | |
| ACCESSION | AF087453 | | | | |
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| REFERENCE | 1 (bases 1 to 4165) Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J. Cloning and Sequencing of the Rattus norvegicus potassium channel KCNO2 | | | | |
| AUTHORS | Unpublished | | | | |
| TITLE | 2 (bases 1 to 4165) Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J. Direct Submission | | | | |
| JOURNAL | Submitted (26-AUG-1998) University of Marburg, Inst. for Physiology, Deutschhausstr. 2, Marburg 35037, Germany 3 (bases 1 to 4165) Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J. Direct Submission | | | | |
| REMARK | Submitted (27-SEP-2001) University of Marburg, Inst. for Physiology, Deutschhausstr. 2, Marburg 35037, Germany Sequence update by submitter On Sep 27, 2001 this sequence version replaced gi:3641299. location/Qualifiers | | | | |
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AUTHORS Wen, H. and Levitan, I. B.
TITLE Calmodulin is an auxiliary subunit of KCNQ channels
REFERENCE 2 (bases 1 to 2613)
AUTHORS Wen, H. and Levitan, I. B.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Neuroscience, University of Pennsylvania,
3450 Hamilton Walk, Philadelphia, PA 19104, USA

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QY 740 LeuValAlaSerLysGluAsnValGlnValAlaGlnSer 752
Db 2422 -----TCCAGGAGAACTGGATGCCCTGGGCGAGC 2451
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Search completed: January 11, 2003, 19:13:06
Job time : 4019 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2003, 16:04:17 ; Search time 298 Seconds
(without alignments)
6710.653 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVSGRRLVLLNSAARG.....SICKAGESTDLSPHYKLR 888

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:
-MODEL=frame+.p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09810796/runal.10012003_085456_22798/app_query.fasta.1.1031
-DB=N.Geneseq.101002 -OFMT=fastlap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsom2 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -COMPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09810796.@cgn.1.1_193_@runal.10012003_085456_22798 -KCPU=6 -ICPU=3
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-NARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|----------|---------------------|
| 1 | 4547 | 100.0 | 2667 | 22 | AA514653 | Human cDNA encoding |
| 2 | 4547 | 100.0 | 2772 | 22 | AAH43633 | Human ion-channel |
| 3 | 4547 | 100.0 | 3111 | 22 | AAH43634 | Human ion-channel |
| 4 | 4527.5 | 99.6 | 2694 | 22 | AA514652 | Human cDNA encoding |
| 5 | 4527.5 | 99.6 | 2694 | 24 | AA027195 | Human potassium ch |
| 6 | 4527.5 | 99.6 | 3137 | 22 | AA085414 | Human KCNQ5 potass |
| 7 | 4523.5 | 99.5 | 3071 | 22 | AA514651 | Human cDNA for vol |
| 8 | 4513.5 | 99.3 | 3074 | 22 | AAH49499 | Human KCNQ5 DNA. |
| 9 | 4346.5 | 95.6 | 3718 | 22 | AA664371 | Human KCNQ5 (KCN6g |
| 10 | 2007.5 | 44.1 | 2335 | 21 | AAA47618 | KCNQ4 potassium ch |
| 11 | 1794 | 39.5 | 3237 | 20 | AA571145 | Human mutant KCNQ2 |
| 12 | 1792.5 | 39.4 | 3287 | 20 | AA526587 | Nucleotide sequenc |
| 13 | 1790.5 | 39.4 | 2169 | 20 | AA526588 | Nucleotide sequenc |
| 14 | 1790 | 39.4 | 2565 | 20 | AA51548 | Human brain-derive |
| 15 | 1790 | 39.4 | 3195 | 23 | AA574831 | DNA encoding novel |
| 16 | 1788 | 39.3 | 3232 | 20 | AA57057 | Human KCNQ2 cDNA. |
| 17 | 1780 | 39.1 | 3232 | 20 | AA574830 | DNA encoding novel |
| 18 | 1775 | 39.0 | 7413 | 23 | AA574832 | DNA encoding novel |
| 19 | 1767 | 38.9 | 2273 | 20 | AA57140 | Mouse KCNQ2 cDNA. |
| 20 | 1762 | 38.8 | 3029 | 20 | AA51547 | Human brain-derive |
| 21 | 1667.5 | 36.7 | 125910 | 21 | AA64370 | Human KCNQ5 (KCN6g |
| 22 | 1587.5 | 34.9 | 2565 | 20 | AA526596 | Nucleotide sequenc |
| 23 | 1587.5 | 34.9 | 2914 | 20 | AA57059 | Human KCNQ3 cDNA. |
| 24 | 1550.5 | 34.1 | 2814 | 20 | AA57141 | Mouse KCNQ3 cDNA. |
| 25 | 1446.5 | 31.8 | 2900 | 22 | AAH99526 | Human protein enco |
| 26 | 1439.5 | 31.7 | 2911 | 23 | AA573267 | DNA encoding novel |
| 27 | 1439.5 | 31.7 | 4154 | 23 | AA583921 | DNA encoding novel |
| 28 | 1248 | 27.4 | 3355 | 22 | AA594798 | Human full-length |
| 29 | 1226.5 | 27.0 | 1182 | 18 | AAH85964 | Human K+ channel g |
| 30 | 1226.5 | 27.0 | 1425 | 24 | ABK64418 | Human beta1g prot |
| 31 | 1116.5 | 24.6 | 3851 | 21 | AA590669 | Human KVLQT1 gene |
| 32 | 1116.5 | 24.6 | 3181 | 21 | AA598901 | Human long QT synd |
| 33 | 1116.5 | 24.6 | 3181 | 21 | AA589911 | Human KVLQT1 codin |
| 34 | 1114 | 24.5 | 2028 | 22 | AA530824 | Human KVLQT1 gene. |
| 35 | 1103.5 | 24.3 | 3182 | 22 | AA589914 | Mutant human KVLQT |
| 36 | 1094 | 24.1 | 2734 | 22 | AA589944 | Mutant human KVLQT |
| 37 | 1094 | 24.1 | 2821 | 18 | AA594004 | DNA encoding human |
| 38 | 1094 | 24.1 | 2821 | 18 | AA594004 | Human KVLQT1 full- |
| 39 | 1094 | 24.1 | 2821 | 24 | ABN96861 | Gene #3359 used to |
| 40 | 1004 | 22.1 | 1280 | 23 | AB128585 | Drosophila melanog |
| 41 | 993.5 | 21.8 | 735 | 20 | AA526589 | Nucleotide sequenc |
| 42 | 976 | 21.5 | 1320 | 23 | AA573266 | DNA encoding novel |
| 43 | 976 | 21.5 | 1320 | 23 | AA583917 | DNA encoding novel |
| 44 | 933.5 | 20.5 | 1566 | 23 | AA567245 | DNA encoding novel |
| 45 | 933.5 | 20.5 | 1566 | 23 | AA584027 | DNA encoding novel |

ALIGNMENTS

RESULT 1
AA514653 standard; cDNA; 2667 BP.

AA514653:
18-DEC-2001 (first entry)

Human cDNA encoding a voltage gated potassium channel hKvN05-2.

Human: ss; voltage-gated potassium channel; KCNQ5-2; nocitropic;
cerebroprotective; neurotropic; analgesic; vision disorder;
central nervous system disorder; epilepsy; migraine; hearing disorder;
psychotic disorder; seizure; learning disorder; memory disorder;
stroke; pain; gene therapy; splice variant.

XX Homo sapiens.
XX OS

QY 421 TTPSerPheasnsAspArgThrArgPheArgProSerLeuArgLeuysSerSerGlnPro 440
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 Db 1261 TGGAGCTTCAACACCGCAACCGCTTCCGCCCTCGCTGGCCCAAAAGTCTCACCCA 1320
 QY 441 LysProValIleAspAlaSerThrAlaLeuGlyThrAspAspValIleArgGlyGly 460
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 Db 1321 AAACCACTGATAGTGGTGCACACGCCCTTGGCCTGATGATGATATGATGAAGAAAGGA 1380
 QY 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
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 Db 1381 TGGCAGTGTGATGATACAGTGAAGACCTCACCCACCACTTAAACTGTCATTGCAAGCT 1440
 QY 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGlyThrLeuArgProLys 500
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 Db 1441 ATCGAATATGAAATTTGATGTTGCAAAACGGAAGTTTAAAGAAAGCTTACGTCATAT 1500
 QY 501 AspValLysAspValIleGluGlnLysSerAlaGlyHisLeuAspMetLeuCysArgIle 520
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 Db 1501 GATTTAAAGATGTGATGAACATATTTCTGCTCATCTGGACATGTTGTGATGAATTT 1560
 QY 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
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 Db 1561 AAAAGCCTTCAACACGCTGTTGATCAAAATTTCTGGAAAGGGCAATCAATCAATCAATAG 1620
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 QY 561 ArgValValLysValGluLysGlnValGlnSerIleGlnSerLysLeuAspCysLeuLeu 580
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 Db 1681 CGGTGTGTCAGAGTTGAAGAAACAGGTACAGTCCATAGAGTCCAAAGCTGACCTACTTA 1740
 QY 581 AspIleTyrglnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
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 Db 1741 GACATCTATCAACAGCTCTTGGGAAAGGCTCTGCTGAGCCCTGCTTGGCTTCATTC 1800
 QY 601 GlnIleProPheGlnCysGlnGlnThrSerAspTyrglnSerProValAspSerLys 620
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 QY 621 AspleuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
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 Db 1861 GATCTTTCGGGCTCGCGCAAAACAGTGGTCTTATCCAGATCAACTAGTCCCAACATC 1920
 QY 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyraIa 660
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 Db 1921 TCGAGAGCCGTCACATTCCTGACGCCAAATGAGTTCAGTCCACAGACTTTCATACGCG 1980
 QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
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 Db 1981 CTTAGCCCTACTATGCAAGTCAACAGCACACAGTGGCCATTAAGTCAAAAGCATGGCTTA 2040
 QY 681 AlaValAlaIleThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaIa 700
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 Db 2041 GCAGTGGCAGCCACCAACCATTCGCAAAACCAATTAATATACGCGACCCCAAGCCACAGCC 2100
 QY 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGlu 720
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 Db 2101 CCAAACAACCTTACAGATCCACCTCTCTCCAGCATTAACCATCTGCCCAGGCCAGAA 2160
 QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnIleSerAspValThrThrCysLeu 740
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 Db 2161 ACTGTGCACCCCAACCTGACAGCTTACGAAAGATTTTCGAGCTCCACCACTGCTT 2220
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 Db 2281 AGGAAAGCTTGTGACATGGGAGAGAAACTCTGTGTCTGTCTCCATGTTGCCGAAG 2340

QY 781 AspleuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGlnLeuAsnIle 800
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 QY 801 GlnLeuSerGlySerGluSerSerGlySerArgLysSerGlnAspPheTyProLysTrp 820
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 Db 2521 ACTTTTGTATGCCCGCACCGCAGCTCCAGGGAAGCTGCTTGCATCAGACTCTCTAAGG 2580
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 ID AAH43633 standard; cDNA: 2772 BP.
 AC AAH43633:
 DT 21-JAN-2002 (first entry)
 DE Human ion-channel forming protein ORF.
 DE Human ion-channel forming protein ORF.
 KM Ion-channel forming protein; voltage-gated potassium channel;
 KW fetal; brain; thymus; prostate; heart; skeletal muscle; probe: ss.
 OS Homo sapiens.
 PN WO200175108-A1.
 PD 11-OCT-2001.
 PF 03-APR-2001; 2001WO-US10875.
 PR 03-APR-2000; 2000US-194255P.
 PA (TEXT-) LEXICON GENETICS INC.
 PI Hu Y, Kieke JA, Turner AC, Nehls WC, Friedrich G, Zambrowicz B;
 PI Sands AT;
 DR WPI: 2001-656987/75.
 DR P-PSDB: ABA47678.
 PT New human ion channel protein and polynucleotides encoding the protein,
 PT useful in diagnosing or treating diseases, in drug screening, and in
 PT clinical trial monitoring
 PS Claim 1: Page 34-35; 41pp; English.
 CC The sequences in AAH43633-34 encode a novel ion-channel forming protein.
 CC The protein shares structural similarity with mammalian ion channel
 CC proteins, particularly voltage-gated potassium channel proteins. The
 CC protein is expressed in many human cell lines including fetal brain,
 CC brain, thymus, prostate, heart and skeletal muscle. The novel protein
 CC can be used in the diagnosis of treatment of diseases, in drug
 CC screening, and in clinical trial monitoring. The oligonucleotides may
 CC be used as hybridization probes for screening libraries, and assessing
 CC gene expression patterns (particularly using a micro array or high
 CC throughput chip format). The nucleic acids and novel protein can also be
 CC used in the identification, selection and validation of novel molecular
 CC targets for drug discovery, to screen collections of genetic material


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OY 641 SerArgGlyLeuGlnPheIleuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
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Db 2566 AGGAAATCCCAATGTTTATTAACGTAGTAAAGAGCGGTGCCGAGAGACAGACAGAC 2625
OY 841 ThrPheAspAlaAlaProGlnProAlaArgGlnAlaIlePheAlaSerAspSerLeuArg 860
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Db 2626 ACTTTTGTATCCCGCAGCGACGCTGCCAGGAGAGCTGCTTTGATCTCAACCTCTTAAG 2685
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ID AAH43634 standard; cDNA; 3111 BP.
XX
AC AAH43634;
XX
DT 21-JAN-2002 (first entry)
XX
DE Human ion-channel forming protein coding sequence.
XX
KW Ion-channel forming protein; voltage-gated potassium channel;
XX fetal; brain; thymus; prostate; heart; skeletal muscle; probe; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 59..2831
XX FT /*tag= a
XX FT /product= "Human ion-channel forming protein"
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PN WO200175108-A1.
PD
XX 11-OCT-2001.
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PF 03-APR-2001; 2001MO-US10875.
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PR 03-APR-2000; 2000US-194255P.
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PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
XX WPI: 2001-656987/75.
DR P-PSDB; AAB47678.
XX
PT New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosing or treating diseases, in drug screening, and in
PT clinical trial monitoring
XX
XX Disclosure: Page 37-38; 41pp; English.
XX
CC The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC The protein shares structural similarity with mammalian ion channel
CC proteins, particularly voltage-gated potassium channel proteins. The
CC protein is expressed in many human cell lines including fetal brain,
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein
CC can be used in the diagnosis or treatment of diseases, in drug
CC screening, and in clinical trial monitoring. The oligonucleotides may
CC be used as hybridization probes for screening libraries, and assessing
CC gene expression patterns (particularly using a micro array or high
CC throughput chip format). The nucleic acids and novel protein can also be
CC used in the identification, selection and validation of novel molecular
CC targets for drug discovery, to screen collections of genetic material
CC from patients who have a particular medical condition, to identify
CC mutations associated with a particular disease, as a diagnostic or
CC prognostic assay, and to screen for drugs which can be used to treat
CC symptomatic or phenotypic manifestations of perturbing the normal
CC function of novel human protein. The polypeptides are further used in
CC generating antibodies.
XX
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Alignment Scores:
Pred. No.: 0 Length: 3111
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
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Db 225 GACGGCTGCTACTGCTGGCGACCCGCGCGCCACGCTCGGTGGCGGGGCGGTGGCTG 284
OY 41 ArgGluSerArgArgGlyIysGlnGlyAlaArgMetSerLeuLeuGlyIysProLeuSer 60
    |||||||
Db 285 AGCGAGAGCGCGCGCGGCAAGCAGGAGGCGCGGATGAGCCCTGCGGAGACCCCTCTCT 344
OY 61 TyrThrSerSerGlnSerCysArgArgAsnValIysTyrArgArgValGlnAsnTyrLeu 80
    |||||||
Db 345 TACACGAGTAGCCAGAGCTCCGCGCAACGTCAAGTACCGCGGGGTGCAGAACTACTCTG 404
OY 81 TyrAsnValLeuGlnArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
    |||||||
Db 405 TACACGCTGCTGAGAGAACCCCGGCGGTGCGTTCACTACACAGCGCTTCTTCTC 464
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[illegible]

| | | | |
|----|------|---|------|
| Db | 1545 | TGCACATGATGATATACAGGGAGAACCTCACCCACACTTAAACTGTCAATTCGAGCT | 1604 |
| QY | 481 | ILLEARGILIEWETLYSPHENISVALAIALYARGLYSPHENYSGUHTHRLAEARGPROTYR | 500 |
| Db | 1605 | ATCAGAAATTATGAATATTCATCTGTCGCAAAACGGAGATTTAAGGAACAATTAAAGTCACATAT | 1664 |
| QY | 501 | ASPVALLYSAPVALLEGLUGINTYRSEARGLYHISLEUASPMECLEUCYSARGILE | 520 |
| Db | 1665 | GATGTAAGAAAGATGTCATTGACACATATTCCTGCTGCATCTGGCAGCAATGTTGTATGAAAT | 1724 |
| QY | 521 | LYSSEIRLEUGLINTHRARYALASPGINILEUGLYLYSGYGINLIETHTSERASPLYS | 540 |
| Db | 1725 | AAAAGGCTTCMAACGGTGGTGAATCAATTCCTGGAAAAGGCAAAATCCATCCAGATGATAG | 1784 |
| QY | 541 | LYSSEARGGLUYLSIETHTRALAGLUHISGLUTHTHRASPALEUSERMETLEUGLY | 560 |
| Db | 1785 | AAGAGCGCGAGAGAAATTAACGACGACAACTGACAGCCACAGACATCTCAGATGCTGGGT | 1844 |
| QY | 561 | ARGVALVALLYSVALGLUYSGINVALGINSERILEGUSERLYSLEUASPCYSLEULEU | 580 |
| Db | 1845 | CGGGGTGGTCAAGGTGTGAAAAACAGGTACACTGCATGAATCCAAAGCTGGAGCTGCTACTA | 1904 |
| QY | 581 | ASPILETYRGINELINALLEUAQLYSGLYSERALASERALLALEUALASERPHE | 600 |
| Db | 1905 | GACATGTATCCAAAGGCTCTCGGAAAAGGTCTGGCCACCCCTGGTGTGGCTTCATTC | 1964 |
| QY | 601 | GLNILEPROPROBHEGLUCYSGUGLINTHRSERAPYRGINSERPROVALASPERLYS | 620 |
| Db | 1965 | CAGATCCCACTTTGATGATGTGAACACACACTCTGACATATCAAAACCCCTGTGGATAGCAA | 2024 |
| QY | 621 | ASPLEUSERGLYSERALAGINASUSERGLYCYLSLEUSERARGSERTHRSEARALASMLE | 640 |
| Db | 2025 | GATCTTTCGGGTTCCGCCACAAACAGTGGCTGCTTATCCAGATCACTAGAGCCCAACATC | 2084 |
| QY | 641 | SERARGLYLEUENLNPHEILEUTHRPASNGLUPHESERLAGINTHRRPHTYRALA | 660 |
| Db | 2085 | TCGAGAGGCGCTGAGTTCATTCTGACCCCAAAATGAGTTCACTGGCCAGACTTCTTACGGC | 2144 |
| QY | 661 | LEUSERPROTHRMETHISSERGINALATHTHGLNVALPROILLESERGINSEARSPGLYSER | 680 |
| Db | 2145 | CTTAGCGCTACTATGACACACTCAAGCAACAAGGTGGCAATTATCAAGCGAATGGCTCA | 2204 |
| QY | 681 | ALAVALALALATHRASNTHRLLEALASNGLILEASNTHRLAPROLYSPROALALA | 700 |
| Db | 2205 | GCAGTGGCAGCCCAACACCATTTGCCAAACCAATAATATCGGCACCCCAAGCCAGCAGCC | 2264 |
| QY | 701 | PROTHRTHLEUENLILEPROPROLEUPROALILELYSHISLEUPROARGPROGLU | 720 |
| Db | 2265 | CCAAACAACCTTTAAGATCCCACTCCCTCCGCCACCATCAAGCAATCTGGCCAGGCCAGAA | 2324 |
| QY | 721 | THLEUHHISPROASNPROALAGLYLEUGLINSERILESEARSPVALTHRTHCYLSLEU | 740 |
| Db | 2325 | ACCTGTGACCCCTAACCTCGCAGGCTTACAGAAAGCATTTCTGACGTCACACCTGCCTT | 2384 |
| QY | 741 | VALALASERLYSGLUASNVALGLINVALAGINSERASNLEUTHRLYSASPARSETMET | 760 |
| Db | 2385 | GTTGCTCCCAAGAAAAATGTTCAAGTTGCACAGTCAATCTCACCAAGAGACGTTCTATG | 2444 |
| QY | 761 | ARGLYSSERPHESPMETGLYGLINTHRLLEUENSERVALCYSPPROMETVALPROLYS | 780 |
| Db | 2445 | AGGAAAGACTTTACATGGGAGGAGAAACCTGTGTCTGTCTGCCATGCTGCCGAAG | 2504 |
| QY | 781 | ASPLEUGLYSSERLEUSERVALGLASNLEULLEARGSERTHRGLINLEUASNMLE | 800 |
| Db | 2505 | GACCTTGGGCAAACTTTGTCTGTGTCAAAACCTGATCTACGCTGACCCGAGGAACATAATATA | 2564 |
| QY | 801 | GLNLEUSERGLYSERGLUSERSERGLYSERARGGLYSERGLNASPHERYRPROLYSTPR | 820 |
| Db | 2565 | CAACTTTCAGGGAGTGATGTCAGAGGCTCCAGAGGAGCCAAAGATTTTACCCCAAAATGG | 2624 |
| QY | 821 | ARGGLUSERLYSLEUPHEILETHRASPGLUGLUVALGLYPROGLUGLINTHRLINTHASP | 840 |

Db 2625 AGGAATCCAAATTTGTTATACATGATGACAGAGGCGGTCCCGAAGACAGACAGACAGAC 2684
QY 841 ThrheaspAlaAlaProGlnProAlaArgIuaAlaIleAlaSerAspSerLeuArg 860
Db 2685 ACTTTGATGCGGACCGACCGCTCCAGGAGAGCTGCTTGCATCAGACTCTTAAGG 2744
QY 861 ThrGlyArgSerArgSerSerGlnSerIleCysIysValaGlyGlnSerThrAspAlaLeu 880
Db 2745 ACTGGAAGGTACAGATCTCTCAGAGACTTTGTAAAGCAGGAATACAGATCCCTC 2804
QY 881 SerLeuProHisValLysLeuLys 888
Db 2805 AGCTTGCTCATGTCAACACTGAAA 2828
RESULT 4
AA514652
ID AA514652 standard; cDNA: 2694 BP.
XX
XX AA514652;
AC
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding a voltage gated potassium channel hKCNQ5-1.
XX
KW Human; ss; voltage-gated potassium channel; hKCNQ5-1; nontropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychologic disorder; seizure; learning disorder; memory disorder;
KW stroke; pain; gene therapy; splice variant.
XX
XX Homo sapiens.
OS
XX
FH key Location/Qualifiers
FT CDS 1..2994
FT /tag= a
FT /product= "hKCNQ5-1"
XX
PN MO2001.0759-A1.
XX
XX 27-SEP-2001.
PF 20-MAR-2001; 2001MO-US09328.
XX
XX 21-MAR-2000; 2000US-190954P.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Jcg1a TJ;
PI
XX
DR WP1: 2001-611467/70.
DR P-PSDB: AAU09020.
XX
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ alpha
PT subunits
PS
PS Claim 5; Page 62-63; 78pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an
CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
CC sequence and forms a KCNQ potassium channel having the characteristic of
CC voltage-gating with at least an additional KCNQ alpha subunit. Also
CC included in the scope of the invention are the nucleic acids encoding
CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
CC expression vectors encoding them, antibodies against them, the use of
CC 3-dimensional computer modeling to identify molecules that bind to a
CC KCNQ containing potassium channel and modulate ion flux through the
CC channel. The KCNQ polypeptide is useful for identifying a compound that
CC increases or decreases ion flux through a potassium channel expressed in
CC an eukaryotic host cell or cell membrane. The compound (and the
CC KCNQ nucleic acid when used in gene therapy) is useful as

CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
CC such as disorders of the central nervous system, such as epilepsy,
CC migraines, hearing and vision problems, psychologic disorders, seizures,
CC learning and memory disorders, stroke and pain. The antibodies are
CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
CC use of a nucleotide sequence of KCNQ5 to search computer databases to
CC find variants of the sequence which are associated with disease states,
CC is useful for screening mutations of KCNQ5. The present sequence is
CC a splice variant of hKCNQ5 encoding hKCNQ5-1.
XX
SQ Sequence 2694 BP: 714 A; 671 C; 669 G; 640 T; 0 other:
XX
Alignment Scores:
Pred. No.: 0 Length: 2694
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 9
Query Match: 99.57% Indels: 0
DB: 22 Gaps: 1
US-09-810-796-5 (1-888) x AA514652 (1-2694)
QY 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAlaArgGly 20
Db 1 ATCAAGAGATGTGAGAGTCGAGCGCGGACGCTGCTGTAACCTCGGACCGCCACGCGC 60
QY 21 AspGlyLeuLeuLeuGlnGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
Db 61 GACGGCGCTCTACTGCTGAGGACCCCGCGGACGCTTGAGGCGCGGCGGCGGCTG 120
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 121 AGGAGACGCCCGCGGACAGCAAGGAGGCGCCGATGAGCTGCTGGGCAAGCGCTCTT 180
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 181 TACACGAGTAGCCAGAGCTGCCGCGCAACGTCAACCTACCGGCGGCTGCAACTACTG 240
QY 81 TyrAsnValLeuGlnArgProArgGlyTyrPAlaPheIleTyrHisAlaPheValPheLeu 100
Db 241 TACACGCTGCTGAGAGACCCCGCGGCTGAGCTTATCTACACCGCTTTCGTTTCTC 300
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 301 CTGTCTTTGGTTGCTTGAATTTTGTCAAGTTTTCACCATCCCTGACGACCAAAATTG 360
QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 361 GCCTCAAGTTGGCTTGTGATCCGAGATTCTGATGATTTGCTCTTTGGTTGGAGTTTC 420
QY 141 IleIleArgIleTyrSerArgIleGlyCysCysArgTyrArgGlyTyrPAlaArgLeu 160
Db 421 ATCATTCGATCTGCTGCTCGGCTTCTGTGTGCAATATAGAGATGAGCAAGAACTG 480
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 481 AGCTTGCTCGAAGAGCCCTTCTGTATATAGATACCATTTGTTTCGTTCAATATAGCA 540
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 541 GTTGTCTTGCAAAATACTCAGGCTAATATTTTGGCACGCTGCACTCGAAGAACTCCCG 600
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyLysThrPyrLysLeuLeu 220
Db 601 TTCTCAAGATCTCTCGCATGGTGGCATGAGACCAAGGAGGAGCACTTGGAAATTACTG 660
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaThrPyrIleGlyPheLeu 240
Db 661 GGTTCAGTGGTTATATGCTACAGCAAGGAATTAATACAGACTTGTAATAGATTTTGG 720
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 721 GTTCTTATTTTTCGTCCTTCTCTCTATCTGTGTAAGAAAGATGCCAATAAAGAGTTT 780

QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
 |||||
 Db 781 TCTTCATATGCAAGATGCTCTCTGCTGGGGCCACAAATTACATTCACATATGCGATGGA 840
 QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
 |||||
 Db 841 GACAAACTCCCTTAACCTGGCTGGAGATGCTTTCTGCAGGGCTTTCACCTCTGGCC 900
 QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
 |||||
 Db 901 ATTTCTTTCTTGGACCTTCGCGGCAATCTGGCTCAGGTTTTCATTAAGATACAA 960
 QY 321 GluGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaAlaAsnLeuIleGln 340
 |||||
 Db 961 GACACACACCCCGCAAAACACTTTGAGAAAGAGAAAGAACCCGCGCTCCACTTCATTCAG 1020
 QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaIleThrTrpLysPro 360
 |||||
 Db 1021 TGTGTTGGCTAGCTTACGCGAGCTGATGAGAAATCTGTTCCATTCAGCAACCTGGAAAGCA 1080
 QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
 |||||
 Db 1081 CACTTGAAGGCTTGACACCTGCAAGCCCTACCAAGAAAGAAAGGAGAGCATCAACG 1140
 QY 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
 |||||
 Db 1141 AGTCAGAAAGCTAACTTTTAAGAGAGGAGTGGCGCATGCTAGCCCGGAGGCGCAGAGTAT 1200
 QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
 |||||
 Db 1201 AAGAGCGCAGCAAGCCTCAGTGGTGACAGGAGGATCCCAAGACCGCAGCATCCACCGCAG 1260
 QY 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
 |||||
 Db 1261 GGCAGTCCCAACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGAAGCCGCTTCGGGCC 1320
 QY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
 |||||
 Db 1321 TGCCTGGCCCTCAAAAGTTCACAGCCAAACAGATGAGATGCTGACACACACCTTGGC 1380
 QY 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
 |||||
 Db 1381 ACTGATGATGATATGATGATAAAGAGATGCCAGTGTGATGATGATGAGAGACCTTACC 1440
 QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
 |||||
 Db 1441 CCACCACTTAAACTGTCATTCGAGCTATCAGAAATTATGAAATTTTCATGTCCAAAAGCG 1500
 QY 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
 |||||
 Db 1501 AAGTTTAAGGAAACGTTACGCCATATGATGATAAAGATGTCATTCAGCAATATTTCTGCT 1560
 QY 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
 |||||
 Db 1561 GGTCACTGTGACATGTTGTGTAGCAATTAAGCCTTCAAAACGCTGTGATCAAAATTTCTT 1620
 QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgLysLysIleThrAlaGlnHisGlu 551
 |||||
 Db 1621 GGAAAGGGCAAAATCAGATCAGATAAGAGAGCCGAGAGAAATATACAGCAGACATGAG 1680
 QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
 |||||
 Db 1681 ACCACAGACGATCTCAGTATGCTCGTGGGTGTCAGAAAGTTGAAAGACAGTACAGTCC 1740
 QY 572 IleGlnSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
 |||||
 Db 1741 ATTAGAGTCCAAAGTGGCTGCTCTACTAGACATTCATCAACAGGCTCTTCGGAAGAGCTCT 1800
 QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGlnCysGlnGlnThrSer 611
 |||||
 Db 1801 GCCTCAGCCCTCGCTTGGCTTCTTCATTCAGATCCACCTTTGATGATGAGACAGACATCT 1860

QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
 |||||
 Db 1861 GACTATCAAAAGCCCTGGATAGCAAAAGATCTTTCGGGTTCCGCAAAAGATGGCTGAC 1920
 QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
 |||||
 Db 1921 TTATCCAGATCACTACTGCGCAACATCTCGAGAGAGCCCTGGAGTTCTATCTCAGCGCAAT 1980
 QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
 |||||
 Db 1981 GAGTTCACTGCCAGACTTCTTACGCGCTTACGCCCTTACTATGACAGATCAAGCAACACAG 2040
 QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
 |||||
 Db 2041 GTGCGCAATTTGTCAAACCGATGCTTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2100
 QY 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 711
 |||||
 Db 2101 ATAAATAGCGCACCCCAAGCCAGAGCCCAACACTTTACAGATCCACCTCTCTCCCA 2160
 QY 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
 |||||
 Db 2161 GCCATCAAGCATCTGCGCCAGCCAGCAAACTCTGCACCTTAACCTTCAGGCTTACAGGAA 2220
 QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
 |||||
 Db 2221 AGCATTTCTACGTCACACACTGCTTGTTCCTCCCAAGAAATGTTTCAGGTTGCACAG 2280
 QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
 |||||
 Db 2281 TCAAAATCTCACCAAGCACCCTTCTATGAGCAAAAGCTTTCATGAGGAGGAGAAACTCTG 2340
 QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
 |||||
 Db 2341 TTGTCTGTCTGCTCCAGTGGCGGAGGACTTGGCAAACTTTGTCTGTGCAAAACCTTG 2400
 QY 792 IleArgSerThrGlnGluLeuAsnIleGlnLeuSerLysSerGlySerGlySerArg 811
 |||||
 Db 2401 ATCAGGTCCAGCCGACGACATGATATACACTTTCAGGAGAGTGTAGTAAAGTGGCTCCAGA 2460
 QY 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 831
 |||||
 Db 2461 GGCAGCCCAAGATTTTAAACCCCAATGAGAGGAGATCCAAATGTTTATTAAGTATGATGAGAG 2520
 QY 832 ValGlyProGlnGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
 |||||
 Db 2521 GTGGTCCCGAAGAGACAGAGACACTTTGTGATGCCACCGCAGCCTGCCAGGGAA 2580
 QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
 |||||
 Db 2581 GCGGCTTTGCATCAGACACTCTCTAAGSACITGGAAGCTCAGACATCATCTCAGACATTTGT 2640
 QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
 |||||
 Db 2641 AAGGCAAGGAGAAAGTACAGATGCCCTCAGCTTCCTCATGTCAAACGTGAAA 2691
 RESULT 5
 AAD27192
 ID AAD27192 standard; cDNA; 2694 BP.
 XX
 AC AAD27192;
 DT 09-APR-2002 (first entry)
 XX
 DE Human potassium channel polypeptide, KCNO5 cDNA.
 KW Human; potassium channel polypeptide; KCNO5; pain; migraine; stroke;
 KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
 KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
 KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
 KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
 KW learning deficiency; cognitive disorder; motor disease; neuron disease;
 KW neuropsychological disorder; neuropsychological disorder; asthma;

Db 1201 AAGAGCCGACAAAGCCTCAGTAGTGACAGAGAGTCCCAAGCAGCATCATCACCAG 1260
 QY 412 GlySerProThrIleValGlnLysSerIlePheAsnAspArgThrArgPheArgPro 431
 Db 1261 GGCGATGCCACCAAGATGTCAGAGAGCTGGAGCTTCAACGACCGAACCCGGCTCCGGCC 1320
 QY 432 SerIleuArgIleuLysSerSerGlnProLysProValIleAspAlaSerThrAlaGluGly 451
 Db 1321 TCGCTGGCCCTCAAAAAGCTTCTCAGCCCAAAACCATGATAGTTCGTGACACAGCCCTTGGC 1380
 QY 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
 Db 1381 ACTGATGATGATATATGATGAAAAAGATGCCAGTGTGATGATCATGAGTGAAGACCTCACC 1440
 QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
 Db 1441 CCACCACTTAAACCTGATTCAGAGTATCAGATATTAATTTCAATGTGCAAAACGG 1500
 QY 492 LysPheLysGluThrIleuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
 Db 1501 AAGTTTAAGGAAAGCTTACGCTCATGATGTAAGATGTCATGACAAATTTCTGCT 1560
 QY 512 GlyHisLysAspMetLeuLysArgIleLysSerLeuGlnThrArgValAspGlnIleu 531
 Db 1561 GGTCATCTGGACATGTTGTGTAATTAAGCCTTCAACACAGCTTGTGTAATTTCTT 1620
 QY 532 GlyLysGlyGlnIlePheSerAspLysLysSerArgGluLysIleThrAlaGluHisGln 551
 Db 1621 GGAAAAAGGCAAAATCACATCATGATAGAAAGCCGAGAAATAATACACAGACATGAG 1680
 QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
 Db 1681 ACCACAGACGATCTCAGATGCTCGTGGGTGGTCAGAGTTGAAACACGATACAGTCC 1740
 QY 572 IleGluSerLysIleuAspCysIleuAspIleTyrGlnGlnValIleuArgLysLysSer 591
 Db 1741 ATAGAGTCCAAAGCTGGAGCTGCTACTAGACATCATCAACAGGCTCTCGGAAAGCTCT 1800
 QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGlnGlnThrSer 611
 Db 1801 GCCCACCACCCCGCTTGGCTTCAATCCAGATCCACCTTTTGAAATGGAACAGACATCT 1860
 QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
 Db 1861 GACATATTAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGACAAACAGAGGCTGC 1920
 QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
 Db 1921 TTATCCAGATCACTAGTGCACATCTCAGAGGCTGCGATTCATTCGACGCCAAT 1980
 QY 652 GluPheSerIleGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
 Db 1981 GAGTTATGTCGCCAGACTTCTACGGCTTACGCCCTACTATGACAGTCAAGCAGACAG 2040
 QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleAsnThrIleAlaAsnGln 691
 Db 2041 GTGGCAATTAGTCAAGGATGGCTCAGCAGTGGCAGCCCAACCACTTGGCAACCAA 2100
 QY 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 711
 Db 2101 ATTAATTAAGGCGCCAGACAGACAGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2160
 QY 712 AlaIleLysHisLeuProArgProGluThrIleuHisProAsnProAlaGlyLeuGlnGlu 731
 Db 2161 GCCATCAAGCATCTGCCAGGCCAGAAACTTGCACCCCTAACCCCTGACAGCTTACAGGAA 2220
 QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaGln 751
 Db 2221 AGCAATTTGACGTCACACACCTGCTTGTGGCTCCAGAGAAAGATTTTCAGGTTCCACAG 2280
 QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGluThrIleu 771
 Db 2281 TCAATATCTACCAAGAGCGTTCTATGAGAAAGCTTTGACATGGAGGAAACCTCTG 2340

QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
 Db 2341 TTGCTGCTGTCCCATGCTGGCCGAAGACATGGGCAATCTTGTCTGTGCAAAACCTG 2400
 QY 792 IleArgSerThrGluGluLeuAsnIleGlnIleuSerGlySerGluSerSerGlySerArg 811
 Db 2401 ATCAGGTGACCGAGGAACTAATATACATCTTACGAGGAGTGAAGTCAAGTGGCTCCAGA 2460
 QY 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGlnGlu 831
 Db 2461 GGCGCCCAAGATTTTACCCCAATGAGGGAATCCAATGTTTATTAAGTGAAGAG 2520
 QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
 Db 2521 GTGGTCCCGAAGACAGACAGACACTTTGATCCCGCAGCAGCTGCCAGGGAA 2580
 QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
 Db 2581 GCTGCCCTTTCATCAGACTCTTAAGACATGGAAGTCAACATCATCTCAGAGCATTTGT 2640
 QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
 Db 2641 AAGCAGAGAAAGTACAGATGCCCTTGCAGCTTGCCTCATGTCAAACTGAA 2691

RESULT 6

ID AAC83414 standard: cDNA: 3137 BP.
 XX AAC85414:

AC AAC85414:
 XX
 DT 20-APR-2001 (first entry)
 XX

DE Human KCNQ5 potassium channel subunit coding sequence.

KW Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
 KW central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
 KW CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
 KW compulsive behaviour; dementia; depression; Huntington's disease;
 KW mania; memory impairment; memory dysfunction; Huntington's disease;
 KW phobia; pick's disease; psychosis; stroke; tremor; seizure; convulsion;
 KW epilepsy; ds.

OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT 1..2694
 FT CDS /*tag= a
 FT /product= "KCNQ5 subunit"

PN WO200077035-A2.
 PN
 XX
 PD 21-DEC-2000.
 PD
 XX

PF 29-MAY-2000: 2000MO-DK00289.

PR 11-JUN-1999: 99DK-0000828.

XX (NEUR-) NEUROSEARCH AS.

XX Jentsch TJ.

DR WPL: 2001-080678/09.

DR P-PSDB: AAB47046.

XX

PT Novel genes encoding KCNQ5 potassium channel subunits, useful for treating Alzheimer's disease, anxiety, ataxia, stroke, dementia.

PT depression, Huntington's disease, schizophrenia and Parkinson's disease

XX

PS Claim 2: Page 44-48; 50pp; English.

CC This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms

CC heteromeric channels with other KCNQ channel subunits, in particular
CC KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
CC chromosome 6 (q44). Chemicals which have the ability to bind to
CC KCNQ5 are useful for diagnosis, treatment, prevention or alleviation
CC of diseases related to diseases or adverse conditions of the central
CC nervous system (CNS), including affective disorders, Alzheimer's
CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
CC neurodegenerative illness, cognitive deficits, compulsive behavior,
CC dementia, depression, Huntington's disease, mania, memory impairment,
CC memory disorders, memory dysfunction, motion disorders, motor
CC disorders, neurodegenerative diseases, Parkinson's disease and
CC Parkinson-like motor disorders, phobias, pick's disease, psychosis,
CC schizophrenia, spinal cord damage, stroke, tremor, seizures,
CC convulsions and epilepsy.

XX Sequence 3137 BP: 865 A; 749 C; 745 G; 778 T; 0 other:

Alignment Scores:

| | | | |
|------------------------|---------|---------------|------|
| Pred. No.: | 0 | Length: | 3137 |
| Score: | 4527.50 | Matches: | 887 |
| Percent Similarity: | 99.00% | Conservative: | 1 |
| Best Local Similarity: | 98.89% | Mismatches: | 0 |
| Query Match: | 99.57% | Indels: | 9 |
| DB: | 22 | Gaps: | 1 |

US-09-810-796-5 (1-888) x AAC85414 (1-3137)

OY 1 MellysaspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGly 20
DB 1 ATGAGAGATGCGAGTGGCGCGGCGAGGGTGTCTGCTGAACTCGCGACCGCGCGGCGC 60
OY 21 AspAluLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
DB 61 GACGGCCGTCTACTGCTGCGACCGCGCGCGCGCGCGCTCGGTGGCGGGGGTGGCTTG 120
OY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 121 AGGAGAGACCGCGCGCGCGAGACGAGGGGCGCGGATGAGCTGTGGGAGACCGCTCT 180
OY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
DB 181 TACACGAGTACCGAGGTGCGCGCGCAACGTCAAGTACCGCGGGGTGCAGAACTACTG 240
OY 81 TyrAsnValLeuGluArgProArgGlyTyrPalaPheIleTyrHisAlaPheValPheLeu 100
DB 241 TACACGCGCTGGAGAGACCGCGCGCGCTGCGCTTCATCTACACGCTTTCGTTTTCT 300
OY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
DB 301 CTGTCTTGTGCTGCTGATTTGTTCAGTGTTCATCCATCCCTGACACACAAATTG 360
OY 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB 361 GCGTCAAGTTCCTTGTATCTGAGAGTTCGTGATGATTCGTCTTGTGGAGTTC 420
OY 141 IleIleArgIleTyrPserAlaGlyCysCysArgTyrArgGlyTyrPalaGlnArgLeu 160
DB 421 ATCAATGCAATCTGGTGGCGGGTTCGCTGTGTGATFAGAGGATGGCAAGGAGACTG 480
OY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 481 AGGTTGTCCGAAGCCCTCTGTGTATAGATACCAATGTTCTTATGCTCAATAGCA 540
OY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 541 GTTGTGTTTGCAGAAACTCAGGGTAAATTTTTCGCCAGCTCGCACTAGAAAGTCTCC 600
OY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
DB 601 TTCTCAGAGATCCTCCGATGGTGGCATGACGAGGAGGAGCACTTGGAAATTTACTG 660
OY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240

DB 661 GCTTCAGTGGTTATGCTCACAGCAAGGAATTAACTACAGCTTGATCATAGATTTTG 720
OY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 721 GTTCTTAATTTTTTGGTCTTCTCTGCTATCTGGGAGAAAGAGCAATTAAGAGTTT 780
OY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrIleGlyTyrGly 280
DB 781 TCTACATTCGACAGATGCTCTGTGGGGGACAAATTCATTGACAACTAATGGCATGCA 840
OY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 841 GACAAACTCCCTCAACTTGGCTGGAGATGCTTCTGCAGCGCTTGCACTCCCTGGC 900
OY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB 901 ATTCTTTCTTGGACCTTCGCGGCAATTCCTGGCTGAGGTTTGGCAATTAAGATACAA 960
OY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 961 GACACACACCGCCCAAAACACTTTCAGAAAGAAAGAACCCAGCTGCCAACCCTCATTCAG 1020
OY 341 CysValTyrPargSerTyrAlaAlaAspLysSerValSerIleAlaThrTrpLysPro 360
DB 1021 TGTGTGGCGTAGTTACGACGCTGATGAAATCTGTTCATTCGCAACCTGGAAAGCA 1080
OY 361 HistLeuLysAlaLeuHisThrCysSerProThr----- 371
DB 1081 CACTGAGAGGCTTCCTACACCTGCGAGCCCTACCAAGAAAGAAAGGAGACATCAAGC 1140
OY 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgLysGlnSerIle 391
DB 1141 AGTCAAGAGCTAAGTTTAAAGAGGAGAGCGCATGGCTAGCCCAAGGGGCGAGAGTAT 1200
OY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGln 411
DB 1201 AAGACCGCAAGACCTCAGTAGTAGACAGGAGCTCCCAAGACCGACATCCACCGCAG 1260
OY 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
DB 1261 GGCAGTCCCAAAAGTGCAGAAAGAGCTGGAGCTTCMACGACCGAACCCTTCGGCGCC 1320
OY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
DB 1321 TCGCGCGGCTCAAAAGTCTCACCACCAACCAAGATAGATGACACACCCCTTGCC 1380
OY 452 ThrAspAspValTyrAspGluLysGlyGlnCysAspValSerValGluAspLeuThr 471
DB 1381 ACTGATGATGTATATGATGAAAGAGATGCCAGTGTGATGATGAGTGAAGACCTCAC 1440
OY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
DB 1441 CCACCACTTAAACGTCTATTGACGTATCAGAAATTTATCAATTTTCATGTCGCAAAACG 1500
OY 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
DB 1501 AAGTTTAAGGAACAATTAACGTCAATATGATGTAAGAAAGATGATTAAGCAAAATTCCT 1560
OY 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
DB 1561 GGTTCATCTGGACATGTGTGTAGAAATTAAGCCTTCAACACGCTGTATCAAAATTC 1620
OY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGlnHisGlu 551
DB 1621 GGAAGAAAGGCAATTCATCAGATCAAGAAAGACCGGAGAAATTAACACAGACATGAG 1680
OY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
DB 1681 ACCACAGACAGATCTCAGTATGCTCGGTGGGTGCAAGGTGAAAGAAACAGGTACAGTCC 1740
OY 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
DB 1741 ATGAGATCCAAAGCTGGAGTGCCTTACTAGCAATCTATCAACAGAGCTCTTCGAAAGGCT 1800


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QY 592 AAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluGluGlnThrSer 611
    |||||||
Db 1801 GCCTCAGGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTCAGACAGACATCT 1860
QY 612 AspTyrGlnSerProValaAspSerLysAspLeuSerGlySerAlaGlnAnsSerGlyCys 631
    |||||||
Db 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTCCGGTTCGACCAAAACAGTGGCTGC 1920
QY 632 LeuSerArgSerThrSerAlaAnsIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
    |||||||
Db 1921 TTATTCAGATCACTAGTGCACACATCTCGAGAGGCTCAGTTCATCTGACGCCAAAT 1980
QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
    |||||||
Db 1981 GAGTTCACTGCCCAAGCTTCTACGGCGTTACCCCTACATGACAGTCAAGACACACAG 2040
QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
    |||||||
Db 2041 GTGCCAATTACTCAAAAGCAGATGGCTCAGCAGTGCAGCCACCAACACCATTCGAAACCA 2100
QY 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
    |||||||
Db 2101 ATTAATACGGACCAACCAACCCAGACCCCAACACTTACAGATCCACCTCCTCCCA 2160
QY 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
    |||||||
Db 2161 GCCATCAAGCATCTGCCAGGCGAGCAAACTCGACCCCTGACAGCTTACAGGAA 2220
QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaGln 751
    |||||||
Db 2221 AGCATTTCTGACGTCACACCTGCTTGTGCTCCCAAGGAAATGTCAGGTGACAG 2280
QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGlnThrLeu 771
    |||||||
Db 2281 TCAATCTCACCAGAGACCGCTTCTATGAGGAAACCTTTGACATGGAGAGAAACTCTG 2340
QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
    |||||||
Db 2341 TTGTCTCTGTCTCCCATGCTGCTCCGAAAGACTTGGCAAACTTTGTCTGTGCAAAACCTG 2400
QY 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlnSerSerGlySerArg 811
    |||||||
Db 2401 ATCAGGTCGACCGAGGAACTTAATATACAACTTTCAGGAGTCAAGTGGCTCCCA 2460
QY 812 GlySerGlnAspPheTyrProLysTrpArgGlnSerLysLeuPheIleThrAspGlnGlu 831
    |||||||
Db 2461 GGCAGCCCAAGATTTTACCCCAATGGAGGAGATCCAAATTTCTTATTAATCATGAAGAG 2520
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
    |||||||
Db 2521 GTGGGTCCCGAAGAGACAGACACTTTGTATGCCGACCCGACCTCCAGGAGAA 2580
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
    |||||||
Db 2581 GCTGCTCTTGCATAGACTCTTAAGGACTGGAAGGTACACATCAATTCAGAGCAATTTGT 2640
QY 872 LysAlaGlyLeuSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
    |||||||
Db 2641 AAGGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2691

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RESULT 7
AAS14651
ID AAS14651 standard; cDNA; 3071 BP.
XX
AC AAS14651;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA for voltage gated potassium channel hKvN05.
XX
KW Human; ss; voltage-gated potassium channel; hKCN05; nootropic;
cerebroprotective; neurotropic; analgesic; vision disorder;

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KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder;
KW stroke; pain; gene therapy.
XX
OS Homo sapiens.
XX
PN WC200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US09328.
XX
PR 21-MAR-2000; 2000US-190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ alpha
PT subunits.
XX
PS Claim 5; Page 61-62; 78pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an
CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
CC sequence and forms a KCNQ potassium channel having the characteristic of
CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
CC included in the scope of the invention are the nucleic acids encoding
CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
CC expression vectors encoding them, antibodies against them, the use of
CC 3-dimensional computer modelling to identify molecules that bind to a
CC KCNQ containing potassium channel and modulate ion flux through the
CC channel. The KCNQ polypeptide is useful for identifying a compound that
CC increases or decreases ion flux through a potassium channel expressed in
CC a eukaryotic host cell or cell membrane. The compound (and the
CC KCNQ nucleic acid when used in gene therapy) is useful as
CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
CC such as disorders of the central nervous system, such as epilepsy,
CC migraines, hearing and vision problems, psychotic disorders, seizures,
CC learning and memory disorders, stroke and pain. The antibodies are
CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
CC use of a nucleotide sequence of KCNQ5 to search computer databases to
CC find variants of the sequence which are associated with disease states,
CC is useful for screening mutations of KCNQ5. The present sequence is
CC a representative cDNA for hKCNQ5.
XX
SQ Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 1 other;

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Alignment Scores:
Pred. No.: 0 Length: 3071
Score: 4523.50 Matches: 886
Percent Similarity: 98.89% Conservative: 1
Best Local Similarity: 98.77% Mismatches: 1
Query Match: 99.488 Indels: 9
DB: 22 Gaps: 1

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US-09-810-796-5 (1-888) x AAS14651 (1-3071)
QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuAnsSerAlaAlaAlaArgGly 20
    |||||||
Db 10 ATCAAGAGATGTGAGTGGGCGCGGAGCGGTGCTGCTGAACTCGCAAGCCGACGAGGCG 69
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
    |||||||
Db 70 GACGCGCTGCTACTGCTGGGACCCGCGGCGCAAGCTTGTGTGGCGGCGGCGGTGCTG 129
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
    |||||||

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| | | | |
|----|------|--|------|
| Db | 130 | AGGAGAGCCCGCCGGGGCAAGCAGAGGGGGCCCGGATGACGCTGCTGGGGGAACCGCTCTT | 189 |
| QY | 61 | TYRTHRSErSeriNserCysArqArqAsnValLysrYrArqArqValGlnAsnTYrLeu | 80 |
| Db | 190 | TACAGGAGTAGGCAGAGCTGCCGGCCCAAGTCAGTACCGGGGGGTGCAGAACTTACTG | 249 |
| QY | 81 | TYrAsnValLeuGluArqProArqGlyTPrAlaPheLleTYrHisAlaPheValPheLeu | 100 |
| Db | 250 | TACAACTGCTGTGAGAGACCCCGCGCTGGCGCTTCATCTACCAACCGCTTCGTTTCTC | 309 |
| QY | 101 | LeuValPheGlyCYsLeuLleLeuSerValPheSerThrLleProGluHisThrLysLeu | 120 |
| Db | 310 | CTTGTCTTGGTGGTCTTGATATTGTGTAGCTTTTGTACACTCCCTGTAGCACAAAAATTG | 369 |
| QY | 121 | AlaSerSerCysLeuLeuLleLeuGluPheValMetLleValPheGlyLeuGluPhe | 140 |
| Db | 370 | GGCTCAGTGGCTCTTGATCCCGAGAGTTCGTATGATGATTCGTGCTTGGTTGGAGTTC | 429 |
| QY | 141 | LleLleArqLleTPrSerAlaGlyCysCysArqTYrArqGlyTPrGlnYrArqLeu | 160 |
| Db | 430 | ATCATTTGCAATCTGGTCTCGCGGCTTCTGTTGTGCATATAGAGATGGCAAGAACTG | 489 |
| QY | 161 | ArqPheAlaArqLYsProPheCysValLleAspThrLleValLleAlaSerLleAla | 180 |
| Db | 490 | AGGTTTGGCGAAAGCCCTTCTGTATAGAACCACTTCTTATCCGCTTCAAATAGCA | 549 |
| QY | 181 | ValValSerAlLYsThrGlnGlnYasnLlePheAlaThrSerAlaLeuArqSerLeuArq | 200 |
| Db | 550 | CTTCTTTTCGCAAAACCTAGAGGTAATATTTTTGGCCACGCTGCACAGAAAGCTCCGT | 609 |
| QY | 201 | PheLeuGlnLleLeuArqMetValArqMetAspArqArqGlyLlyThrTPrLysLeuLeu | 220 |
| Db | 610 | TTCTCATAGATCCTCCGCATCGTGGCGATAGACCAAGGAGGACTTGGAAATTACTG | 669 |
| QY | 221 | GlySerValValTYrAlaHisSerLYsGluLeuLleThrAlaTPrLYrLleGlyPheLeu | 240 |
| Db | 670 | GGTTCAGTGGTTATGCTCACACCAAGAAATTAATCACACTTGGTCAATAGATTTTGTG | 729 |
| QY | 241 | ValLeuLlePheSerSerPheLeuValTYrLeuValGluLysAspAlaAsnLYsGluPhe | 260 |
| Db | 730 | CTTCTTATTTTTTCGCTTTCCTTGTCTATCTGTGGAAAAAGATGCCAATAAGACTTT | 789 |
| QY | 261 | SerThrTYrAlaAspAlaLeuTPrTPrGlyThrLleThrLeuThrThrLleGlyTYrGly | 280 |
| Db | 790 | TCTACATATGCAAGATGCTCTCTGTGGGGCAATTCATTTGACAACTATGCTCATGGA | 849 |
| QY | 281 | AspLYsThrProLeuThrTPrPheGlyArqLeuLeuSerAlaGlyPheAlaLeuGly | 300 |
| Db | 850 | GACAAACCTCCCTAATCTTGGCGGAGAAAGTTCTTCTCAGGCTTTGGCACTCTTGGC | 909 |
| QY | 301 | LleSerPhePheAlaLeuProAlaGlyLleGlnGlySerGlyPheAlaLeuLYsValGln | 320 |
| Db | 910 | ATTCTCTTTTGGCACTTCTCTGGCGCATTTCTTGCTCAAGTTTGCAITTAAGTACAA | 969 |
| QY | 321 | GluGlnHisArqGlnLYsHisPheGluLYsArqArqAsnProAlaAlaAsnLeuLleGln | 340 |
| Db | 970 | GAAACAACCCCGCAGAAACACTTGGAGAAAGAAAGAACCCAGCTGCCAACCCTATTCAG | 1029 |
| QY | 341 | CysValTPrArqSerSerYrAlaAlaAspGluLYsSerValSerLleAlaThrTPrLYsPro | 360 |
| Db | 1030 | TGTGTGTGGCGTAGTACCCAGCTGTAGAAATACTGTTCATTCGAACCTGGAAACCA | 1089 |
| QY | 361 | HisLeuLYsAlaLeuHisThrCYsSerProThr----- | 371 |
| Db | 1090 | CACTTGAAGGCTTGCAACCTGCAGCCCTACCAAGAAACAAAGGGAAGCATCAAC | 1149 |
| QY | 372 | AsnGlnLYsLeuSerPheLYsGluArqValArqMetAlaSerProArqGlyGlnSerLle | 391 |
| Db | 1150 | AGTCAGAACTAAGTTTAAAGAGCGAGTCCGATGCTAGCCCCAGGGGCCAAGATATT | 1209 |
| QY | 392 | LYsSerArqGlnAlaSerValGlyAspArqArqSerProSerThrAspLleThrAlaGlu | 411 |
| Db | 1210 | AAGAGCCGCAAGCCCTCACTAGTGTGACAGAGAGTCCCAAGCAACCGCATCACAGCCAG | 1269 |

| | | | |
|----|------|---|------|
| QY | 412 | GLYSerProThrLysValGlnLysSerTTPSerPheAsnAspArgThrArgPheArgPro | 431 |
| Db | 1270 | GGCAGGCCCAACAAAGTGGCGAAGAGGTGGAGGCTTCAACGACCAACCCGCTTCGGCGCC | 1329 |
| QY | 432 | SerLeuArgLeuLysSerSerGlnProLysProValIleAspIleAspThrAlaLeuGly | 451 |
| Db | 1330 | TGGCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTCGTAATGCTGCACAGCCCTTGGC | 1389 |
| QY | 452 | ThrAspValLysArgSpGlnLysGlyCysGlnCysAspAlaSerValGluAspLeuThr | 471 |
| Db | 1390 | ACGATGATGTATATGATGATAAAGATGGCAGGTGATGTATGATGAGGAAGACTCAC | 1449 |
| QY | 472 | ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg | 491 |
| Db | 1450 | CCACCACTTAAACCTGATTCAGAGTATCGAATTTGAAATTTCAATGTTGCAAAACGG | 1509 |
| QY | 492 | LysPheLysGlnThrLeuArgProThrAspValLysAspValIleGlnGlnTyrSerAla | 511 |
| Db | 1510 | AGGTTTAAAGAAACRTTACCTCATATGATGATGAAGTGAACATGCAATTGAACAATATTCT | 1569 |
| QY | 512 | GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu | 531 |
| Db | 1570 | GGCATCTGGCACTGTTGTTGTAGATTTAAAGCCTTAAACACCTGTTGATCAAAATCTT | 1629 |
| QY | 532 | GlyLysGlyGlnIleThrSerAspLysLysSerArgLysIleThrAlaGlnHisGln | 551 |
| Db | 1630 | GGAAAGGCGCAATTCATCATGATTAAGAAAGCGCGAAGAAATTAACAGCAGCAATGAG | 1689 |
| QY | 552 | ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGlnLysGlnValGlnSer | 571 |
| Db | 1690 | ACCACAGACGATTCAGTATAGCTCGCGGTGGTCAAGGTGAAAAACAGTCACAGTCC | 1749 |
| QY | 572 | IleGlnSerLysLeuAspCysLeuLeuAspIleArgGlnGlnValLeuArgLysGlySer | 591 |
| Db | 1750 | ATAGATTCACAGCTGGAGCTGCCACTAGACATGATCATACAGAGTCCTTGGAAAGGCT | 1809 |
| QY | 592 | AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlnCysGlnThrSer | 611 |
| Db | 1810 | GGCTCAGCCCTCCCTTGGCTTATTCACGTTCCACCTTTGATGTGAACACACATCT | 1869 |
| QY | 612 | AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys | 631 |
| Db | 1870 | GACTATCAAAAGCCCTGTGATTAGCAAAAGATCTTTCGGGTTCCGCACAAACAGTGGCTCC | 1929 |
| QY | 632 | LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn | 651 |
| Db | 1930 | TTCATCCAGATCACTAGTGCACACATCTCGAAGAGGCTCGAGTCAATTCTGACGCCAAT | 1989 |
| QY | 652 | GlnPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln | 671 |
| Db | 1990 | GAATTCAGGCCCCAGACTTCTACGGGCTTAGGCCCTACTGTGCACTGCAAGCAACACAG | 2049 |
| QY | 672 | ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln | 691 |
| Db | 2050 | GTCGCATTAAGTCAAAAGCGATGGCTCGACAGTGGCAGCACCAACACCATTTGCCAAACAA | 2109 |
| QY | 692 | IleAsnThrAlaProLysProAlaIleAlaProThrThrLeuGlnIleProProLeuPro | 711 |
| Db | 2110 | ATTAATAACGGCACCAAGCAGCAGCCCAACAACCTTTACAGATCCCACTCCCTCCCA | 2169 |
| QY | 712 | AlaIleLysHisLeuProArgProGlnThrLeuHisProAsnProAlaGlyLeuGlnGln | 731 |
| Db | 2170 | GCCATTAAGCATTTGCCCGAAGCAAACTGTGACCCCTTAACCTGAGGCTTACAGGAA | 2229 |
| QY | 732 | SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaGln | 751 |
| Db | 2230 | AGCATTTTCGACGTCACACACTGCTTGTGGCTCCAAAGAAATGTTTCAGGTTGCACAG | 2289 |
| QY | 752 | SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGlnThrLeu | 771 |
| Db | 2290 | TCAAATCTCACCAAGAGACGCTTATGAGAAAAAGCTTTGACATGGGAGGAAACACTCTG | 2349 |

Db 995 TCCTCATATGACAGATGCTCTGTGGGGGCACAAATTACATTGCACAATAATTGGCTATGCA 1054
Oy 281 AsplystrProLeuThrTrpLeuGlyValrLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1055 GACAAACATCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGGCACTCTTGGC 1114
Oy 301 IleSerPhePheAlaLeuProAlaGlyLLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1115 ATTCTCTTCTTGGCACTTCCCTGGCGCATCTTGGCTCAGGTTTGCATTAATACTACAA 1174
Oy 321 GluGlnHisAlaGlnLysHisPheGlnLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1175 GAACAACACCCCGCAAACTTTGAGAAAGAGGAAGCAACCCAGCTGCCAACCCTCAATTAG 1234
Oy 341 CysValTrpArgSerTyrAlaAlaAspGlnLysSerValSerIleAlaThrTrpLysPro 360
Db 1235 TGTGTTGGCGTAGTACCGCAGCTGATGAGAAATCTGTTTCATTGCCAACCTGGAAAGCA 1294
Oy 361 HisLeuLysAlaLeuHisThrCysSerProThr 371
Db 1295 CACTTGAAGGCTTGGACACCTGGACGCCCTACCAAGAAAGAAAGGGAAGCATCAAGC 1354
Oy 372 AsnGlnLysLeuSerPheLysGlnArgValArgMetAlaSerProArgGlyInsIle 391
Db 1355 AGTCAGAAAGCTAAGCTTTTAAAGAGAGAGAGTGGCAGCTAGCCCGAGGGCCAGAGTATT 1414
Oy 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGln 411
Db 1415 AAGAGCCGACAAAGCTCGTAGTACGACAGAGTCCCAAGCAGCCGACATCCACAGCCGAG 1474
Oy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1475 GGCAGTCCACCAAGTGCAGAGAGCTGGAGCTTCACAGCAGCCGACCCGCTCCGGCCC 1534
Oy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1535 TCAGTGGCCCTCAAAAGTTCTCAGCCAAACACAGTAGATGCTGACACAGCCCTTGCC 1594
Oy 452 ThrAspAspValTyrAspGlnLysGlyCysGlnCysAspValSerValGlnAspLeuThr 471
Db 1595 ACTGATGATGATATGATGAGAAAGAGATGCCAGTGTGATGATACGTGGAGACCTCACC 1654
Oy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1655 CCACCACCTAAACCTGTCATTCAGAGCTATCAGAAATTATGAATAATTTCATTCAGAAACGG 1714
Oy 492 LysPheLysGlnThrLeuArgProTyrAspValLysAspValIleGlnGlnTyrSerAla 511
Db 1715 AAGTTTAAAGGAACATTAAGTCCATATGATGATTAAGATGTCATTGAACAAATATCTGCT 1774
Oy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1775 GGTGATCGGACATGTTGTGTAGAAATTAAGCCCTTCAACACGCTGTTGCAAAATTTCTT 1834
Oy 532 GlyLysGlnGlnIleThrSerAspLysLysSerArgGlnLysIleThrAlaGlnHisGln 551
Db 1835 GGAAGAGGGCAAAATCAGATCAGATAGAGAGCCGAGAGAAATTAACAGCAACATGAG 1894
Oy 552 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGlnLysGlnValGlnSer 571
Db 1895 ACCCAGACGATCTCAGATGCTGGTGGGTGGTCAAGGTTGAAAACAGGTACAGTCC 1954
Oy 572 IleGlnSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1955 ATGATATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGCTCTTCCGGAAGGCTCT 2014
Oy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGlnCysGlnGlnThrSer 611
Db 2015 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACACTTGAATGTGAACACAGCATCT 2074
Oy 612 AspLysGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyLys 631
Db 2075 GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGGGTTCCGACAAACAGTGGCTGC 2134

Oy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 2135 TTATCCAGATCACTAGTGTCCACACATCTTCGACAGGCTCCAGTTCTTTCAGCCCAAT 2194
Oy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 2195 GAGTTCAGTGGCCAGACTTCTTACGGGGCTTACCCCTACTATGCACAGTCACAGCAACAG 2254
Oy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
Db 2255 GTGCCAATTATGCAAAAGCATGCTCAGCAGTGCAGCCACCAACACCATTCCAAAACCA 2314
Oy 692 IleAsnThrAlaProLysProAlaIleProThrThrLeuGlnIleProProProLeuPro 711
Db 2315 ATAAATTCGCGACCCCAAGCAGCAGCAGCCCAACACTTACAGATCCCACTCTCTCCCA 2374
Oy 712 AlaIleLysHisLeuProArgProGlnThrLeuHisProAsnProAlaGlyLeuGlnGln 731
Db 2375 GCCATCAAGCATCTGCCCGAGGCGCAAACTCTGCACACCTTAACCTGGCAGGCTTACAGGA 2434
Oy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaGln 751
Db 2435 ACCATTCTGACGTACACACCTGCTTGTGGCTCCCAAGGAAATCTTCAGGTTCCACAG 2494
Oy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyValGlnThrLeu 771
Db 2495 TCAAATCTCACCAGGACCGCTCTATGAGGAAAGCTTTGACATGGAGAGCAAACTCTG 2554
Oy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
Db 2555 TTGCTGTGTCGTCCCATGGTGGCGAAGACTTGGGCAAACTTTTGCTGTGCAAAACCTG 2614
Oy 792 IleArgSerThrGlnGlnLeuAsnIleGlnLeuSerGlySerGlnSerSerGlySerArg 811
Db 2615 ATCAGGTGACCGAGGAACTGATATACAACTTTCAGGAGAGTCAAGTGGCTCCAGA 2674
Oy 812 GlySerGlnAspPheTyrProLysTrpArgGlnSerLysLeuPheIleThrAspGlnGln 831
Db 2675 GGCACCCAAAGATTTTATCCCCCAATGGAGAGGAAATCCAAATTTTATATAGTCATGAAG 2734
Oy 832 ValGlyProGlnGlnThrGlnThrAspThrPheAspAlaAlaProGlnProAlaArgGln 851
Db 2735 GTGGCTCCCGAAGACAGACAGACACTTTTGTATGTCGCGCACCCGACGCTCCAGGGA 2794
Oy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleGly 871
Db 2795 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGTCAACGATCATCTCAGAGCATTTGT 2854
Oy 872 LysAlaGlyGlnSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db 2855 AAGCAGCAGGAAGATACAGATGCTCCCTCACTGCTTCATGTCAAACTGAAA 2905
RESULT 9
AAC64371
ID AAC64371 standard: cDNA: 3718 BP.
XX AAC64371:
AC
XX 07-FEB-2001 (first entry)
DT
XX
XX
DE Human KCM65 (KCM6q) cDNA sequence SEQ ID NO:2.
XX
XX Human: KCM65: KCM6q: chromosome 6: voltage-gated potassium channel;
KW Stargardt-like macular dystrophy: cone rod macular dystrophy;
KW Salla disease: ophthalmological; auditory; central nervous system;
KW cardiocative; anticonvulsant; gastrointestinal; muscular active;
KW age-related macular degeneration; macular degeneration; deafness;
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW gastrointestinal disorder; ss.
XX
XX Homo sapiens.
OS

PN W0200061606-A1.
 XX 19-OCT-2000.
 XX 10-APR-2000; 2000MO-US09587.
 PF 14-APR-1999; 99US-0129274.
 XX (MERI) MERCK & CO INC.
 PA Petrunkhin K, Caskey CT, Li W, Metzker ML;
 PI WPI: 2000-647417/62.
 XX P-PSDB; AAB24241.
 DR Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
 XX
 PS Claim 3; Fig 2; 99pp; English.
 CC The present sequence encodes the human KCNQ5 (also called KCN6q)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardioactive, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q.
 XX
 SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 3718
 Score: 4346.50 Matches: 850
 Percent Similarity: 98.84% Conservative: 1
 Best Local Similarity: 98.72% Mismatches: 1
 Query Match: 95.59% Indels: 9
 Gaps: 1
 US-09-810-796-5 (1-888) x AAC64371 (1-3718)
 QY 37 GlyIyGlyLeuAArgGluSerAArgArgIyGlnGlyAlaArgMetSerLeuEngly 56
 DB 93 GGGCGTGGCCCTGAGGAGAGAGCGCGGGGCAAGAGGGGGCCGATGAGCCCTGGGG 152
 QY 57 LysPProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgVal 76
 DB 153 AAGCGCGCTCTTACACAGAGTAGCCAGAGCTGCCGCGCAAGCTCAAGTACGCGGGGTG 212
 QY 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTrrAlaPheLeuThrHisAla 96
 DB 213 CAGAACTACCTGTCACAGAGTGGAGAGACCCCGCGGCTGGGCTTCATCTACCGAGCT 272
 QY 97 PheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGlu 116
 DB 273 TTGCTTTTTCCTTCCTGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 332
 QY 117 HisThrLysLeuAlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValAlaPhe 136
 DB 333 CACACAAATGCGCTCAAGTTGCTCTTGATCTGAGATGCTGATGATGATGATGATGAT 392
 QY 137 GlyLeuGluPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 156
 DB 393 GGTGGTGGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 452
 QY 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle 176
 DB 453 CAAGAGAGACGTGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 512

QY 177 AlaSerIleAlaValAlaSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
 DB 513 GCTTCATATACAGTGTGCTTTCGCAAAAACTCAGGGTAATATTTTGGCCAGCTGCACTC 572
 QY 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThr 216
 DB 573 AGAGTCTCCGTTTCTTACAGATCTCCGATGGTGGCATGGAGCCAGAGGGAGGCACT 632
 QY 217 TrpLysLeuLeuGlySerValIleTyrAlaHisSerLysGluLeuIleThrAlaTrpTyr 236
 DB 633 TGGAAATTTACGGGTTCAGTGTGTTATGCTCACAAGCAAGATTAATACAGCTTGATAC 692
 QY 237 IleGlyPheLeuValIlePheSerSerPheLeuValIleTyrLeuValGluLysAspAla 256
 DB 693 ATAGGATTTTGGTCTTATTTTTCCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 752
 QY 257 AsnLysGluPheSerThrTrrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThr 276
 DB 753 AATTAAGAGTTTCTTACATATGACATGCTCTGCTGGGGGACAAATTACATTGACACT 812
 QY 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
 DB 813 ATTGGCTATGGAGCAAAACTCCCTTAACCTGGCTGGGAGATTGCTTTCGACAGCTTT 872
 QY 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
 DB 873 GCACCTCTTGGCATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 932
 QY 317 LeuLysValGlnGluGlnHisArgGluLysHisPheGluLysArgArgAsnProAlaAla 336
 DB 933 TTAAATATACAGACACACACCCGACAGAACCTTTGAGAAAAGAGAGACCCAGCTGCC 992
 QY 337 AsnLeuIleGlnCysValIleTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAla 356
 DB 993 AACCTCATTCAGTGTGTTGGCTAGTTACACGACTGATGAGAAATGTTTCCATTGCA 1052
 QY 357 ThrTrpLysProHisLysLysAlaLeuHisThrCysSerProThr 371
 DB 1053 ACCTGAGAGCCACCTTGAAGCCCTTGCACACCTGCACCCCTTACCAGAAAGACAGAG 1112
 QY 372 -----AsgLysLysSerPheLysGluArgValArgMetAlaSerProArg 387
 DB 1113 GAAGCATCAACCACTCAACACTTAAGTTTAAAGACGACGATGCCATGCCATGCCACAG 1172
 QY 388 GlyLysSerIleLysSerArgGlnAlaSerValGlyAspArgSerProSerThrAsp 407
 DB 1173 GGCAGAGTATTAAGACCGCAGCAAGCCTCAGTAGGTGACAGAGGTCCCAAGCACGAC 1232
 QY 408 IleThrAlaGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThr 427
 DB 1233 ATCACACCGGAGGCACTCCACCAAAAGTGCAAGAGCTGGAGCTTTCACGCCGAAC 1292
 QY 428 ArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAsp 447
 DB 1293 CGCTTCCGGCCCTGCTGCGCTCAAAAGTTCTCAGCCAAAACAGTATATGATGCTGAC 1352
 QY 448 ThrAlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerVal 467
 DB 1353 ACAGCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1412
 QY 468 GluAspLeuThrProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHis 487
 DB 1413 GAAGACCTCACCCACACACTTAAACAGTCAATTCGAGCTATACAGATATATCAAAATTTAT 1472
 QY 488 ValAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGlu 507
 DB 1473 GTTGCAGAGCGAGGTTTAAGAGAACATTTACGTCATATGATGATGATGATGATGATG 1532
 QY 508 GlnTyrSerAlaGlnHisLysAspMetLeuCysArgIleLysSerLeuGlnThrArgVal 527
 DB 1533 CAATATTCGTGCTGATCATGAGACATGTTGCTGATGAATTAAGGCTTCAAAACAGCTGT 1592

QY 528 AspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgLysIleThr 547
 |||
 |||
 Db 1593 GATCAATCTTGGAAAAAGGCAATCATCATGAAGAAGAGCCGAGAAATATACA 1652
 QY 548 AlaGluHisIuThrThrAspAspLeuSerMetLeuGlyAtrgValValLysValLys 567
 |||
 |||
 Db 1653 GCAGAACATGAGACACAGAGATCTCAGTAWGCTCGGTGCGGTGTCAGAGTTGAAAAA 1712
 QY 568 GluValGlnSerIleGlnSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeu 587
 |||
 |||
 Db 1713 CAGGTACAGTCCATAGATATCCAGCTGACTGCTACTAGCATCTATCAACAGGCTCTT 1772
 QY 588 ArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGlnCys 607
 |||
 |||
 Db 1773 CGGAAAGGCTCTGCTCAGCCCTGCTTGGCTTCATTCCAGATCCACCTTTGAATGT 1832
 QY 608 GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGln 627
 |||
 |||
 Db 1833 GAACAGACATCTACTATTCAAAGCCCTGTGATAGCAAAAGATCTTTCGGTTCCGACAA 1892
 QY 628 AsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgLysLeuGlnPheIle 647
 |||
 |||
 Db 1893 AACAGTGGCTGCTTATTCACATCATCACTAGTCCAAACATCTCGAAGAGCCTGCAGTTCATT 1952
 QY 648 LeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSer 667
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 |||
 Db 1953 CTGACGCCAATGAGTTCACTGACGCTGCTTACGCGCTTAGCCCTACTATGACACAGT 2012
 QY 668 GlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThr 687
 |||
 |||
 Db 2013 CAAGCAACACAGGCGCAATTAGTCAAAAGCATGCTCAGACAGGCGACCAACCAACCC 2072
 QY 688 IleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIlePro 707
 |||
 |||
 Db 2073 ATTGCAAACCAATTAATACGGCCACCAGCCAGACAGCCCAACACTTTACAGATCCCA 2132
 QY 708 ProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAla 727
 |||
 |||
 Db 2133 CCTCCTCTCCACCATCATGACATCTGCTCCAGGCGCAAACTGTGACCTTAACCTTCA 2192
 QY 728 GlyLeuGlnGlnSerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnVal 747
 |||
 |||
 Db 2193 GGGCTTACGAGAAAGCATTTTGCAGTCACACCTGCTGTTGGCTCCCAAGAAATGT 2252
 QY 748 GlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGly 767
 |||
 |||
 Db 2253 CAGGTTCACAGTCAATTCACCAAGAGCCGTTCTATGAGAAAGCTTTGACATGGGA 2312
 QY 768 GlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSer 787
 |||
 |||
 Db 2313 GGAGAAACTGTGTCTGCTGCTGCTCCATGGTGGCGAAAGCACTTGGCAAAATCTTGTCT 2372
 QY 788 ValGlnAsnLeuIleArgSerThrGluLeuAsnIleGlnLeuSerGlySerLysLeuSer 807
 |||
 |||
 Db 2373 GTGCAAAACCTGATCAGGTGACCGAGGAAGTGAATATACACTTTCAGGAGTGAGTCA 2432
 QY 808 SerGlySerArgLysSerGlnAspPheTyrProLysTyrArgGlnSerLysLeuPheIle 827
 |||
 |||
 Db 2433 AGTGCTCCAGAGGAGCCCAAGATTTTACCCCAATGAGAGGAATCCAAATGTTTATA 2492
 QY 828 ThrAspGlnGluValGlyProGlnGluThrGluThrAspThrPheAspAlaAlaProGln 847
 |||
 |||
 Db 2493 ACTGATGAAGAGGTGGTCCCGAAAGACAGACAGACACTTTGATGGCCGACCCGAG 2552
 QY 848 ProAlaArgGluAlaAlaPheAlaSerAspSerLeuArgThrGlnArgSerArgSerSer 867
 |||
 |||
 Db 2553 CCGGCAAGGAGAACTGCTTGCATCAGACTCTTAAGAGCTGAAGGTGACAGATCACT 2612
 QY 868 GlnSerIleCysLysAlaGlyLysLeuThrAspAlaLeuSerLeuProHisValLysLeu 887
 |||
 |||
 Db 2613 CAGAGCATTTGTAAAGCAGAGAAAGATACAGATGCCCTCAGCTTGCTCAAACTG 2672
 QY 888 Lys 888

Db 2673 AAA 2675
 |||
 RESULT 10
 AAA47618
 ID AAA47618 standard; cDNA; 2335 BP.
 AC AAA47618;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE KCNQ4 Potassium channel gene.
 XX
 KW KCNQ4: potassium channel; cardiac arrhythmia; neonatal epilepsy;
 KW deafness; probes; treatment; therapy; transgenic animal; antibody;
 KW agonist; antagonist; flunitus; hearing loss; neonatal deafness;
 KW presbycusis; affective disorder; compulsive behavior; dementia;
 KW ataxia; cognitive deficits; Huntington's disease; mania; memory impairment;
 KW depression; Huntington's disease; mania; memory impairment;
 KW motor disorders; neurodegenerative disease; Parkinson's disease;
 KW Pick's disease; psychosis; schizophrenia; spinal cord damage;
 KW stroke; tremor; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 83..2170 /tag_a
 FT /product= KCNQ4 Potassium channel polypeptide
 FT
 PN WO200044786-A1.
 XX
 PD 03-AUG-2000.
 XX
 PE 19-JAN-2000; 2000MO-DK00024.
 XX
 PR 26-JAN-1999; 99DK-0000076.
 PR 19-MAY-1999; 99DK-0000693.
 XX
 PA (NEUR-) NEUROSEARCH AS.
 XX
 PI Jentsch TJ;
 DR P-PSDB; AAB01476.
 XX
 PT Nucleic acids encoding the novel KCNQ4 potassium channel subunit,
 PT useful e.g. for treating flunitus, deafness, Alzheimer's and
 PS Parkinson's diseases
 PS
 XX
 Claim 1: Page 43-48; 65pp; English.
 CC Mutations in 3 known genes of the KCNQ branch of the potassium
 CC channel gene family underlie inherited cardiac arrhythmia's, neonatal
 CC epilepsy and in some cases associated with deafness. KCNQ4 has been
 CC mapped to the DFNA2 locus for autosomal dominant hearing loss, and
 CC a dominant negative KCNQ4 mutation that causes deafness in a DFNA2
 CC pedigree has been identified. KCNQ4 is the first potassium channel
 CC gene underlying non-syndromic deafness. KCNQ4 forms heteromeric
 CC channels with other KCNQ channel subunits, especially KCNQ3.
 CC Nucleotides encoding the KCNQ4 protein and the protein itself may be
 CC used in the prevention, treatment and diagnosis of diseases
 CC associated with inappropriate KCNQ4 expression. The nucleotides may
 CC also be used as DNA probes in diagnostic assays (e.g. polymerase
 CC chain reactions (PCR)) to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples and to identify mutations
 CC within them, and hence which patients may be in need of restorative
 CC therapy. They may also be used to study the expression and function
 CC of KCNQ4 polypeptides and their role in metabolism, for example
 CC through the production of transgenic animals. The KCNQ4 polypeptides
 CC may be used as antigens in the production of antibodies and to
 CC identify modulators (agonists and antagonists) of KCNQ4 expression
 CC and activity. The anti-KCNQ4 antibodies and KCNQ4 antagonists may

CC also be used to down regulate KCNQ4 expression and activity. They may
 CC be used in this way to treat tinnitus, loss of hearing (especially
 CC progressive hearing loss, neonatal deafness and presbycusis
 CC (deafness of the elderly)) and disease or adverse conditions of the
 CC central nervous system (CNS) such as affective disorder, Alzheimer's
 CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
 CC neurodegenerative illness, cognitive deficits, compulsive behavior,
 CC dementia, depression, Huntington's disease, mania, memory impairment,
 CC memory disorders and dysfunctions, motion disorders, motor disorders,
 CC neurodegenerative diseases, Parkinson's disease, Parkinson-like motor
 CC disorders, phobias, Pick's disease, psychosis, schizophrenia, spinal
 CC cord damage, stroke and/or tremor. Conversely, antisense nucleic acid
 CC molecules may be administered to down regulate KCNQ4 expression by
 CC binding with the cells own KCNQ4 genes and preventing their
 CC expression.

XX Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 other;

Alignment Scores:

| Pred. No.: | 1-76e-161 | Length: | 2335 |
|------------------------|-----------|---------------|------|
| Score: | 2007.50 | Matches: | 434 |
| Percent Similarity: | 65.32% | Conservative: | 82 |
| Best Local Similarity: | 54.94% | Mismatches: | 133 |
| Query Match: | 44.15% | Indels: | 141 |
| | | Gaps: | 16 |

US-09-810-796-5 (1-888) x AAA47618 (1-2335)

QY 8 ArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeuLeuGly 27
 Db 127 CGGGAGACCCCGCCGCGAGCTAGTGGCTCAGCGC----- 165
 QY 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlnSerArgArgGlyLys 47
 Db 166 --CGTGAGAGCGAACAAGGCGAGCGGG-----CGGGGCGG 201
 QY 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59
 Db 202 CTCGCCGCGCGGCTCTGCGGAGCTGCGGCGCGCGCGCGCGCGCTCCCTGG 261
 QY 60 -----SerTyThrSerSerGlnSerCysAlaArgAsnValLysTy 73
 Db 262 GCCGGGCTCCGCGCTCCGCTCCGCTCCGCGCGCGCGCGCGCGCGCGCGCTA 321
 QY 73 ArgArgGlyAlaGlnAsnTyLeuTyAsnValLeuGlnArgProArgGlyTyrAlaPheI 93
 Db 322 CCGCGGCTGCAAGACTGGGTCTACACGCTGCGGAGCGGCGCGCGGCTGCTTCT 361
 QY 93 eTyHisAlaPheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerTh 113
 Db 382 CTACACGCTTCATATTTTGTGCTGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCT 441
 QY 113 rIleProGlnHisThrLysLeuAlaSerSerCysLeuLeuIleLeuGlnPheValIle 133
 Db 442 TATCCAGAGACCAAGCACTTCCACACAGTGTCTCCATCTTGAATTCGTGATGAT 501
 QY 133 eValValPheGlyLeuGlnGlnPheIleLeuArgTLeuPheSerAlaGlyCysCysArgTy 153
 Db 502 CGTGGTTTCGCGCTTGGAGTACATGCTCGGGGTGGTGGTGGTGGTGGTGGTGA 561
 QY 153 rArgGlyTyrPheGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrI 173
 Db 562 CCGAGAGATGGAGGAGGCTCGCTTCCGTTGGCCAGAAAGCCCTTCTGTGTCATGCTCAT 621
 QY 173 eValLeuIleAlaSerIleAlaValAlaSerAlaLysThrGlnGlyAsnIlePheAlaTh 193
 Db 622 CGTGTCTGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 681
 QY 193 rSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgAr 213
 Db 682 GTCCGCGCTGGCGACATGCTTCCTGCGATCCCTGCGCATGGTGGATGGACCGCGG 741
 QY 213 gGlyGlyThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGlnLeuLeuTh 233

Db 742 CGGGGACACCTGGAGAGCTGCGGCTCAGTGTGTACGCGCATACAGAGACTATAC 801
 QY 233 rAlaTrpTyrIleGlyPheLeuValIlePheSerSerPheLeuValTyrLeuValI 253
 Db 802 CGCCTGGTACATCGGATTCCTGCTGCTCATCTTCCCTCCCTCGGCTACCTGGCGCA 861
 QY 253 uLysAspAlaAsnLysGlnPheSerThrTyrAlaAspAlaLeuTrpTyrGlyThIleTh 273
 Db 862 GAAGAGCGCAACTCCGACTTCTCTCTACGCGCATCTGCTGGTGGGAGCATATAC 921
 QY 273 rLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeu 293
 Db 922 ATTACACAACCTGGCTGTGTGTGACACACACCGACATGCTGGCGAGGCTCTGGC 981
 QY 293 rAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySe 313
 Db 982 TGTGGCTTCGCTTACGCGGATCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTG 1041
 QY 313 rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGlyLysArgArgAs 333
 Db 1042 CGGCTTGGCTTGAAGTTCAGAGACAGACCGCGAGACACTTTCGAGAAAGCGAGGAT 1101
 QY 333 nProAlaAlaAsnLeuIleGlnCysValTyrPheSerTyrAlaAlaAsp---GluLysSe 352
 Db 1102 GCCGCGACCGACCTCATCCAGCGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTG 1161
 QY 352 rValSerIleAlaThrTrp----- 358
 Db 1162 CTACCTGACACCGCACCTGCTACTATGACAGTATCTCCCATCTTCAGAGACTGGC 1221
 QY 358 ----- 358
 Db 1222 CTTTGTGTGAGCAGTGCACAGGCGCGGCGGAGGCGCTACGCGCTGGAGGTGG 1281
 QY 359 -----LysProHisLeuLysAlaLeuHisTh 367
 Db 1282 GCGGGGCGCGGTACCCGAGAGACACCTCCCGTTACCGCGCGCTGGCACCTGGCACCG 1341
 QY 367 r-----CysSerProThrAsnGlnLysLeuSerPheLysGlnArgVa 381
 Db 1342 GCCGAGGACGACCTCTTCTCTGCTGCGGAAAGCGCGCGGATGGGCATCAAGACCGCAT 1401
 QY 381 rArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----AlaSerValG 399
 Db 1402 CCGCATGGGACGCTCCGCGGCGGAGCGGCTCTTCAAGCAGCAGCTGGCACCTTCAAC 1461
 QY 399 yAspArgArgSerProSerThrAspIleThrAlaGlnGly---SerProThrLysValG 418
 Db 1462 AATGCCACCTCCCAAGACAGCAGAGAGTGGGTGAGGCCACACCGCCACCAAGAGTGA 1521
 QY 418 nLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuAlaGlyLeuSerSe 438
 Db 1522 AAAAGAGCTGAGCTTCAATGACCCGCGCTTCCGGGCACTCTCGAAGACTC----- 1573
 QY 438 rGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspI 458
 Db 1574 -----AAACCCCGCACCTTGTGTGAGATGCC---CCCTCAGAGGAATGACAGAGA 1623
 QY 458 uLysGlyCysGlnCysAsnLysSerValGlnAspLeuThrProProLeuLysThrValI 478
 Db 1624 GAACAGCTACACAGTGTGAGTCCAGCGGTGAGACATCATGCTGCTGTGAAGACAGTCA 1683
 QY 478 eArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGlnThrLeuAr 498
 Db 1684 CCGCTCATCGAGATTCCTCAAGTCTGCTGGTCCCAAAAGAAATTCAGAGGAGACCTGG 1743
 QY 498 gProTyrAspValLysAspValIleGlnGlnTyrSerAlaGlyHisLysAspMetLeuCy 518
 Db 1744 ACCGTACAGCTGAAGAGCGCATTTGAGCACTACTCACAGAGCCACCTGGACATCTGG 1803
 QY 518 sArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlnIleThrSe 538

QY 350 -----GlySerValSerIleAlaThrTrpLys----- 359
 Db 1132 TCCAGTGGAGTACTAGAGGAGGTCACCGTCCCACTGACAGTTCCGCAAACTCAA 1191
 QY 360 -----ProHisLeuLysAlaLeuHisThr----- 367
 Db 1192 ACCTACGGGGCTCCAGACTTATCCCCCGGTGAACACGTGAGCTCTGTGAAACCTC 1251
 QY 367 ----- 367
 Db 1252 AAGATAAATCTGAGCTGCTTTACGAGAGACCCCCCGGAGCCGCTCCAAATAA 1311
 QY 368 -----CysSerPro-----ThrAsnGlnLysLeu 375
 Db 1312 GGCAGCCCGTCAGAGAGGCCCTGTGTGATGCTGCCCGGACCGCTTCAGCCAGAAAGTTC 1371
 QY 376 SerPheLysGlnArgValArgMetAlaSerProArgGlnSerIleLysSerArgGln 395
 Db 1372 AGTTTGAAGAATCTGTC---TTCTCAGCCCCCGAGCGCTGCTGCCAAGGAGGAGG 1428
 QY 396 AlaSerValLysP-----ArgArgSerProSerThrAspIleThrAlaGlnLysSer 413
 Db 1429 TCCCCGAGCCGACAGACTGAGCGGCTCAACCCGCGCCAGACAGCTTCGAGAGACAGC 1488
 QY 414 ProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeu 433
 Db 1489 CCCAGCAAGGCTGCCAAGAGCTGAGGCTTCGGGAGCCGCGGAGCCGAGCCGAGCTTTC 1548
 QY 434 ArgLeuLysSerSerGlnProLysProValIleAspAlaSerPheAlaLeuGlnLysThr 453
 Db 1549 CGCATCAAGGCTCGCGGCTCAGCCGAG-----AACTCAAGACCAAGCCCTCCCGGAGAG 1602
 QY 454 AspValLysAspGlnLysGlnLysGlnCysAspValSerValGlnLysLeuProPro 473
 Db 1603 GACATTGTGATGACAAAGAGCTCCCTCGAGTTGTGACGAGGACCTGAGCCCGGCG 1662
 QY 474 LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe 493
 Db 1663 CTCGAAGTGCATGACATGACACCGCTGTGTATGCTGCTGCTGCTGCTGCTGCTGCTG 1722
 QY 494 LysGlnThrLeuArgProTrpArgAspValLysAspValIleGlnLysSerAlaGlnHis 513
 Db 1723 AAGGAGAGCTCGCGCCCTACGACGATGATGAGATGATGATGATGATGATGATGATGATG 1782
 QY 514 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAlaAspGlnIleLeuGlnLys 533
 Db 1783 CTGACATGCTGTCTCCGAAATTAAGACCTGACGTCAGAGTGCAGACAGATCTGGGGCGG 1842
 QY 534 GlnGlnIleThrSerAspLysLysSerArgGlnLysIleThrAlaGlnHisGlnThrThr 553
 Db 1843 GGCCCGAGATCAGCGAC---AAGGACCGCACCAAGGCGCCGCGGAGCGGAGCTGCC 1899
 QY 554 AspAspLeuSerMetLeuGlnArgValValLysValGlnLysGlnValGlnSerIleGln 573
 Db 1900 GAGGACCCGACATGATGATGAGCGCTCGGAAAGGTGAGGAGGAGGAGGAGGAGGAGG 1959
 QY 574 SerLysLeuAspCysLeuLeuAspIleTrpGlnGlnValLeuArgLysGlnSerAlaSer 593
 Db 1960 AAGAAGCTGGACTTCTCGTGAATATCTACATGCAAG-----CGATGGGC----- 2004
 QY 594 AlaLeuAlaLeuAlaSerPheGlnIleProPheGlnLys----- 607
 Db 2005 -----ATCCCCCGACAGACAGACGAGCGCTACTTGGGGCC 2040
 QY 608 -----GlnGlnThrSerAspTrpGlnSerProValAspSerLysAspLeuSerLys 624
 Db 2041 AAGAGCCCGGAGCGCGCGCGCTGACACAGCCCGGAGACACCGGAG----- 2091
 QY 625 SerAlaGlnAsnSerGlnCysLeuSerArgSerThrSerAlaAsnIleSerArgGlnLeu 644
 Db 2092 CATGTCGACAGGACGCTCATTTGCAAGATGCTGCGCTCCAGCACTCCACGCGC--- 2148
 QY 645 GlnPheIleLeuThrProAsnGlnPheSerAlaGlnThrPheTrpAlaLeuSerProThr 664

Db 2148 ----- 2148
 QY 665 MetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaIa 684
 Db 2148 ----- 2148
 QY 685 ThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeu 704
 Db 2149 -----CAGAAAGACTTCTCGGCGCCCGCGCGCGCC---CCGTCTC 2187
 QY 705 GlnIleProPro----- 2187
 Db 2188 CAGTGTCCGCTCCCTACCTCTGCGAGCCAGACCCCGCGC---CCAGGGCCAGGAGC 2246
 QY 716 LeuProArg-----ProGlnThr-----LeuHis-ProAsnProAlaGlnLysGlnI 731
 Db 2247 CTCCCGCTGGGGGACCAAGCTCTCCGTGTCGATCCCGCGCGCTCCCGCCAGAGCG 2306
 QY 731 uSerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaG 751
 Db 2307 GTGCTGTCCGCTACAGCGGCGGACACCGCGCCAGATGAGTTCTGCGGAGAGAG 2366
 QY 751 nSerAsnLeuThrLys-----AspArgSerMetArgLysSerPheAspMetGlyGly 769
 Db 2367 CACCCCGGCTGACAGGCCCGCCCGAGGGAGCCCTGCGGAGACAGC-----GA 2411
 QY 769 uThrLeuLeuSerValCysProMetValProLysAspLeuGlnLysSerLeuSerValG 789
 Db 2412 CAGCTGCATCTCCATCCGCTGCGTGCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2471
 QY 789 nasnLeuIleArgSerThrGlnGlnLeuAsn 799
 Db 2472 CAGCATCTCCCACTCCAGAGAGAACTGAT 2502
 RESULT 13
 AAX26588
 ID AAX26588 standard; DNA; 2169 bp.
 XX
 AC AAX26588;
 XX
 DT 16-JUN-1999 (first entry)
 XX
 DE Nucleotide sequence of murine KCNQ2 (formerly known as (KvLRL).
 XX
 KW KCNQ protein; nervous system-specific potassium channel;
 KW neuronal excitability; neurotransmitter release; KCNQ modulator;
 KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
 KW age-associated memory loss; learning deficiency; motor neuron disease;
 KW epilepsy; stroke; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2169
 FTT /*tag= a
 PN MO9907832-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 26-JUN-1998; 98MO-US13276.
 XX
 PR 12-AUG-1997; 97US-0055599.
 XX
 PA (BRIM) BRISTOL-MYERS SQUID CO.
 XX
 PI Bjanar MA, Dworetzky S, Gridkov V, Levesque PC;
 PI Little WA, Neubauer MG, Yang W;
 XX
 DR WPI: 1999-190047/16.
 DR P-PSDB: AAY01530.

Db 712 ATGGCTTCCTCTGCCCTCATCCTGGCCTCATTTTCTGGTACTTGGCAGAAAGGGTGA

1780 CCCCTCGGAGGTGGAGAAACAGGCTTGTCCATGGAAAAGAGCTCGACTTCTTGGTG

| | | | |
|-----------|-------------|---|------|
| Qy | 581 | AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe | 600 |
| Db | 1840 | AGCATATCAACACAG-----AGATGGC----- | 1863 |
| Qy | 601 | GlnIleProPheGlnCys----- | |
| Db | 1864 | ---ATCCACACAGACAGACAGAGGCTATTTTGGGCCAAGAGCCGTGACCCGCACCA | 1920 |
| Qy | 612 | AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys | 631 |
| Db | 1921 | CCCTACACACAGCCACAGAGACAGCCGTGAC-----CATGCAGACAAACATGCGCTGT | 1971 |
| Qy | 632 | -----LeuSerArgSerThrSerAlaAsnLeuSerArgGlyLeuGlnPheIleLeu | 648 |
| Db | 1972 | ATCATTAAGATGCTCGCTCCACACACTCT----- | 2001 |
| Qy | 649 | ThrProAsnGlnPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGln | 668 |
| Db | 2002 | -----ACGGGCCACAGAGAACTACGACAGACCCACAGCATC-----CCC | 2040 |
| Qy | 669 | AlaThrGlnValProIleSerGlnSer | 677 |
| Db | 2041 | CCTGCCAGCTGTCTCTCCCTCCACACTCG | 2067 |
| RESULT 14 | | | |
| ID | AAx81548 | standard; DNA; 2565 BP. | |
| AC | AAx81548; | | |
| DT | 25-AUG-1999 | (first entry) | |
| XX | | | |
| DE | | Human brain-derived potassium channel DNA structural DNA. | |
| KW | | Human: brain-derived potassium channel; neurophysiology; | |
| KW | | cognitive disorder; behavioural disorder; psychiatric disorder; | |
| KW | | neurodegenerative disorder; developmental disorder; mental retardation; | |
| KW | | asthma; migraine; epilepsy; stroke; brain tumour; Huntington's disease; | |
| KW | | Lou Gehrig's; neurodegeneration; multiple sclerosis; psychosis; | |
| KW | | amyotrophic lateral sclerosis; retinitis pigmentosa; | |
| KW | | cerebellar degeneration; urinary incontinence; diabetes; asthma; | |
| KW | | premature labour; hypertension; cardiac ischaemia; arrhythmia; | |
| KW | | autoimmune disease; cancer; graft rejection; inflammation; allergy; | |
| KW | | proliferative disorder; anaemia; autoimmune disease; | |
| KW | | Type-1 diabetes mellitus myasthenia gravis; systemic lupus erythematosus; | |
| KW | | Sjogren's syndrome; mixed connective tissue disease; | |
| KW | | experimental allergic encephalomyelitis; rheumatoid arthritis; ss. | |
| XX | | | |
| OS | | Homo sapiens. | |
| PN | | W09931232-A1. | |
| XX | | | |
| PD | | 24-JUN-1999. | |
| XX | | | |
| PF | | 11-DEC-1998; 98WO-GB03720. | |
| XX | | | |
| PR | | 13-DEC-1997; 97GB-0026339. | |
| XX | | | |
| PA | | (ZENEC) ZENECA LTD. | |
| XX | | | |
| PI | | Aiyar J, Christian EP, Iannotti CA, Logsdon NJ; | |
| XX | | | |
| DR | | WPI; 1999-395178/33. | |
| XX | | | |
| PT | | New isolated potassium channel polypeptide | |
| XX | | | |
| PS | | Claim 2; Fig 2; 151pp; English. | |
| XX | | | |
| CC | | The present sequence represents brain-derived potassium channel DNA. | |
| CC | | The polynucleotides and polypeptides can be used for identifying | |
| CC | | compounds that modulate the biological activity of a potassium channel | |
| CC | | or neurophysiology. It is used as a method of treatment for patients | |
| CC | | with conditions which are mediated by the biological activity of a | |

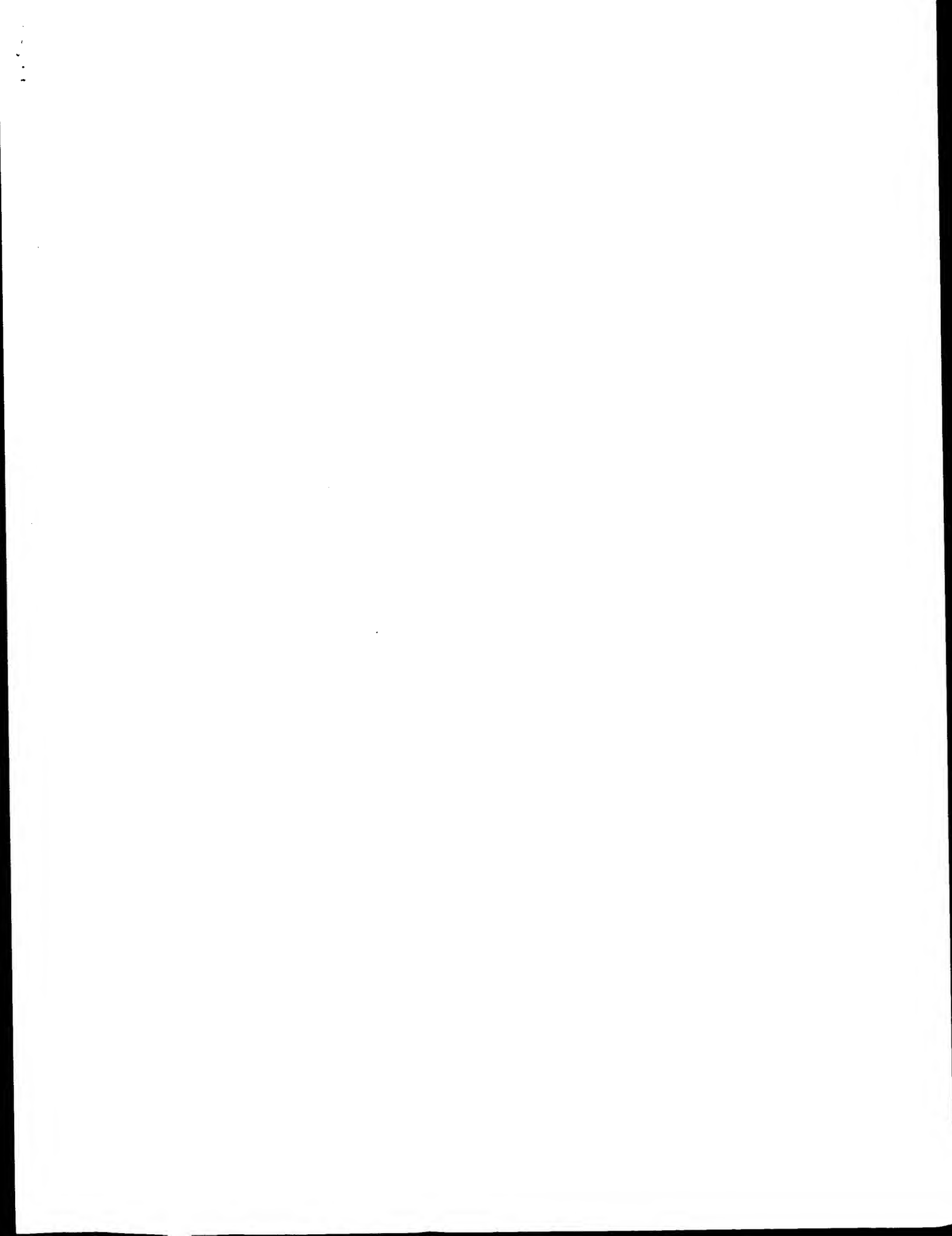
| Seq | Sequence | 2565 BP; 474 A; 846 C; 818 G; 427 T; 0 other; |
|---|--|---|
| CC | human potassium channel. Antagonists can be used in modulating cognitive | |
| CC | behavioral, psychiatric, neurodegenerative and developmental disorders | |
| CC | (mental retardation) as well as asthma, migraine, epilepsy and stroke | |
| CC | and brain tumors. They can be used for treating diseases such as | |
| CC | Huntington's disease, Lou Gehrig's, neurodegeneration, multiple | |
| CC | sclerosis, psychosis, amyotrophic lateral sclerosis, retinitis | |
| CC | pigmentosa, cerebellar degeneration, urinary incontinence, diabetes, | |
| CC | asthma, premature labour, hypertension, cardiac ischaemia and arrhythmias, | |
| CC | autoimmune diseases, cancer, graft rejections, acute and chronic | |
| CC | inflammation, allergies, proliferative disorders, anemias, | |
| CC | neurodegenerative diseases with immunological components, as well as | |
| CC | autoimmune diseases including rheumatoid arthritis, type-1 diabetes | |
| CC | melittus, myasthenia gravis, systemic lupus erythematosus, Sjogren's | |
| CC | syndrome, mixed connective tissue disease, and experimental allergic | |
| CC | encephalomyelitis (EAE). | |
| XX | | |
| XX | | |
| SO | Sequence 2565 BP; 474 A; 846 C; 818 G; 427 T; 0 other; | |
| Alignment Scores: | | |
| | Pred. No.: | 8.07e-143 |
| | Score: | 1790.00 |
| | Percent Similarity: | 59.84% |
| | Best Local Similarity: | 48.13% |
| | Query Match: | 39.37% |
| DB: | | |
| | Length: | 2565 |
| | Matches: | 411 |
| | Conservative: | 100 |
| | Mismatches: | 183 |
| | Indels: | 161 |
| | Gaps: | 22 |
| US-09-810-796-5 (1-888) x AAX81548 (1-2565) | | |
| QY | 17 AAlaAargGlyAspGlyLeuLeuLeuLeuGlyThrArgAlaAthrLeuGlyGly | 36 |
| DB | 100 TCCACCGGGAGCGGGGCGTGTGATGGCCGGCTCCAGGCCCCAACG-----CGC | 150 |
| QY | 37 GylGlyGlyLeuAargGlySerAargArgGlyLysGlnGlyAlaArgMetSerLeuGly | 56 |
| DB | 151 GCGACGACCTCTGAGAACCTCGCGCGGGCGCGCGCGCC-----GGG | 195 |
| QY | 57 LysProLeuSerTyrrThrSerSerGlnSerCysArgArgAspValLysTyrrArgArg | 76 |
| DB | 196 AAGCCC-----CCCAACGCAAGCGCTTCACGCAAGCTG | 231 |
| QY | 77 GlasprrTyrrLeuTyrrAsnValLeuGluAargProAargLysTyrrAlaPheLeuTyrrHis | 96 |
| DB | 232 CACAAATTCTCTACAAACGGCTGGAGCGCGCGCGCGTGGCGCTCATCTACACAGCC | 291 |
| QY | 97 PheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerThrLeuProGlu | 116 |
| DB | 292 TACGTGTCTCTCTGTGTTTCTCTGCGCTCGTGTCTGTCTTTTCCACATCAAGAG | 351 |
| QY | 117 HistThrLysLeuAlaSerSerCysLeuLeuLeuGluPheValMetLeuValValPhe | 136 |
| DB | 352 TATGACAAAGCTCGGAGGGGCGCTTCACACATCGGAATCTGTACATATCGTGTGTT | 411 |
| QY | 137 GlyLeuGluPheLeuLeuLeuArgLLeuPserAlaGlyCysCysArgTyrrArgLys | 156 |
| DB | 412 GCGGTGGAACTACTGTGTGGGATCGGGCCGAGGCTCTCTGCGGTACCGTGG | 471 |
| QY | 157 GlnGlyArgLeuAargPheAlaArgLysProPheCysValLeuAspThrLeuValLeuLeu | 176 |
| DB | 472 ACGGGCGGCTCAATTGGCCGGAAACGTTGTGTGTGATGACATCATGAGTCTCATC | 531 |
| QY | 177 AlaSerIleAlaValAlaSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu | 196 |
| DB | 532 GCGTCCATTGGGTCGTGGCGCGCGGCTCCAGGCAACGCTTTGCCACATCTGGGCTC | 591 |
| QY | 197 ArgSerLeuAargPheLeuGlnIleLeuAargMetValAargMetAspAargGlyGlyThr | 216 |
| DB | 592 CGGACCGCGCTCTCTGACAGATTCTCGGATATCCGCATGTGACCGGGAGGACAC | 651 |
| QY | 217 TrpLysLeuLeuGlySerValValTyrrAlaHisSerLysGlnLeuLeuLeuThrAlaTrp | 236 |
| DB | 652 TGGAAAGCTGTGGGCTCTGTGTCTATGCCCAACGACAGAGCTGGTCACTGCTGTGAC | 711 |
| QY | 237 IleGlyPheLeuValIleuIlePheSerSerThrAlaValValValValValValVal | 711 |

| | | | |
|----|------|--|------|
| OY | 117 | HisThrLysLeuAlaSerSerCysLeuLeuIleLeuGlnAlaMetIleValIlePhe | 136 |
| | 118 | | 137 |
| Db | 527 | TATGAGAAAGAGCTGGAGGGGGCCCTCATATCTCTGAAATCTGACTATCGTGGT | 586 |
| OY | 137 | GlyLeuGlnAlaPheIleIleArgIleTyrPheSerAlaGlyCysCysGlyArgTyrArgIleTyr | 156 |
| | 138 | | 139 |
| Db | 587 | GGCGTGAAGTACTCGTCGGGAGTCTGGCGCCGAGCGTGGCTGGCGGTAACCTGGCTGG | 646 |
| OY | 157 | GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValIle | 176 |
| | 158 | | 159 |
| Db | 647 | AAGGGGCGGCTCAAGTTGGCCCGGAAACCGTTCTGTCATTGACATCATGGTGCATC | 706 |
| OY | 177 | AlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu | 196 |
| | 178 | | 179 |
| Db | 707 | GGCTTCATTGGCGTCTGGCGCCGGCTCCAGGGCCACAGTCTTGGCCATCTGGCGTC | 766 |
| OY | 197 | ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgIleGlyThr | 216 |
| | 198 | | 199 |
| Db | 767 | CGAGACCTTCGGCTCTCTGCAGATTCTGGGAGATCCGATGACCGGGGGAGGACAC | 826 |
| OY | 217 | TryPheLeuLeuGlySerValValTyrAlaHisSerLysGlnLeuIleThrAlaTyrTyr | 236 |
| | 218 | | 219 |
| Db | 827 | TGGAAAGCTGGGGGTCTGGTGTATATCCACACAGCAAGAGACCTGGTCACTGCCGTAC | 886 |
| OY | 237 | IleGlyPheLeuValIleIlePheSerPheLeuValTyrLeuValGlnLysAspAla | 256 |
| | 238 | | 239 |
| Db | 887 | ATCGGCTTCCTTGTGTCTATCTATCTGGCGCTCGTTCCTGGTGTACTGGGACAGAAAGGGGAG | 946 |
| OY | 257 | AsnLysGlnPheSerThrTyrAlaAspAlaLeuTyrPheGlyThrIleThrLeuThrThr | 276 |
| | 258 | | 259 |
| Db | 947 | AACACACACTTTCAGACCTTACCGGATGCACTGTGGTGGGCGTATACCTGACCCAC | 1006 |
| OY | 277 | IleGlyTyrGlyAspLysThrProLeuThrTyrPheGlyArgLeuLeuSerAlaGlyPhe | 296 |
| | 278 | | 279 |
| Db | 1007 | ATTGGCTACGGGGGCAAGTACCCCCAGACCTGGAGCGGACGGCTTCGGCGCAACCTTC | 1066 |
| OY | 297 | AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla | 316 |
| | 298 | | 299 |
| Db | 1067 | ACCCTCATCGGTGCTCTCTTCTGGCGCTCGCTCAGGCACTTGGGGTCTGGGTTGGC | 1126 |
| OY | 317 | LeuLysPheAlaGlnGlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaAla | 336 |
| | 318 | | 319 |
| Db | 1127 | CTAAGAGTTTGAAGAGCAGCAGACGCAAAACACTTTGAGAAGGCGGAACCCGCGACGA | 1186 |
| OY | 337 | AsnLeuIleGlnCysValTyrPheSerTyrAlaAlaAsp----- | 349 |
| | 338 | | 339 |
| Db | 1187 | GGCTGATCCAGTCGGCGCTGCAATTCTACGCCACCACTCTTCGGCCACAGACTGGCAC | 1246 |
| OY | 350 | -----GlnLysSerValSerIleAlaThrTyrLys----- | 359 |
| | 351 | | 352 |
| Db | 1247 | TCCACGTGCAGTACTACGAGCAGCAAGCGTACCGTCCCATGTACAGTTGGCAACTCAA | 1306 |
| OY | 360 | -----ProHisLeuLysAlaLeuHisThrCys----- | 368 |
| | 361 | | 362 |
| Db | 1307 | ACCTACGGGGCTCCAGACTTATCCCGCGCTGAACCACTGTGAGCTGAGAGAACTTC | 1366 |
| OY | 369 | -----SerProThrAsn----- | 372 |
| | 370 | | 371 |
| Db | 1367 | AAGAGTAATCTGCACTCGCTTTCAGGAAGGAAACCCCCCGGAGCGGCTCTCCA---AAC | 1423 |
| OY | 373 | GlnLysLeuSerPheLysGlnLysValArgMetAlaSerProArgLysIleSerIleLys | 392 |
| | 374 | | 375 |
| Db | 1424 | CAGAAGGTCAAGTTGAAAGATGGTGTTC---TTCCTCAGGCCCGGAGGGCTGGCTGGCAG | 1480 |
| OY | 393 | SerArgGlnAlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAla | 410 |
| | 394 | | 395 |
| Db | 1481 | GGGAAGGGGTCCCCCGACGCCCAAGCACTGTGAGGGCGGTACCCAGGCGCGCAAGAGCCTC | 1540 |
| OY | 411 | GlnGlySerProThrLysValGlnLysSerTyrPheAsnAspArgThrArgPheArg | 430 |
| | 412 | | 413 |
| Db | 1541 | GAGAGACACCCCGACAAAGGTGCCCAAGAGCTGGAGACTTCGGGGACCGACGCGGGCACGC | 1600 |
| OY | 431 | ProSerLeuArgLeuLysSerSerClnProLysProValIleAspAlaAspThrAlaLeu | 450 |

Db 1601 CAGGCTTCCGATCAAGGGTGGCCGCTCAAGGAGACACTCAGAA---GAAGCAAGGCTC 1657
QY 451 GLTThraspsvalYTraspgIuLySgIncysaspValSerValGluaspLeu 470
Db 1658 CCGGAGAGAGCATTTGGATGACAAAGAGCTGCCCTCAGAGTTTGTGACCGAGACTG 1717
QY 471 ThrProLeuLeuYThrValIleArgAlaIleArgIleMetLysPheHisValAlaLys 490
Db 1718 ACCCGCGGCTCAAAAGTCACATCAGACATCAGACCGGTGTGTCTCATGGCTTCGAGTCCAG 1777
QY 491 ArgLysPheLysGluThrLeuArgProTyTraspValLysaspValIleGluGlnTyTrSer 510
Db 1778 CGGAAGTTCAGAGAGAGAGCTGCGGCTCAGACGTGTGACGTCATCGAGCACTACTCA 1837
QY 511 AlaGlyHisLeuaspMetLeuGlyArgIleLysSerLeuGlnThrArgValaspGlnIle 530
Db 1838 GCGGCGCACTGACATGCTGCTCCGAAATTAAGAGCTTCAGTCCAGAGTGCACAGATC 1897
QY 531 LeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHis 550
Db 1898 GTGGGGCGGGGCCACCATCAAGGAC---AAGGACCGCACCAAGGGCCCGCGGAGGCG 1954
QY 551 GluThrThrAspaspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGln 570
Db 1955 GAGCTGCCCGGAGAGACCCCGATGATGAGGAGCGCTCGGAGAGTGGAGAAGAGTCTTG 2014
QY 571 SerIleGluSerLysLeuaspPcysLeuLeuaspIleTyrlngInValLeuArgLysGly 590
Db 2015 TCCATGAGAGAAAGACTGACTTCTGTTGAATATCTACATCAG---CGATGGGC 2068
QY 591 SerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCys----- 607
Db 2069 -----ATCCCCCGCAGAGAGACCGAGGCTTAC 2095
QY 608 -----GluGlnThrSerAspTyrlngInSerProValaspSerLysasp 621
Db 2096 TTTGGGGCCAAAGAGCCGGAAGCGCGGCCGCTACACAGCCGAGACAGCGGAG 2155
QY 622 LeuSerGlySerAlaGlnasnSerGlyLysSerArgSerThrSerAlaasnIleSer 641
Db 2156 -----CATGTCGACAGCAGCGGCTGCATTTGTCAAGATCGTGGCTCCAGCAGCTCC 2206
QY 642 ArgGlyLeuGlnPheIleLeuThrProasnGluPheSerAlaGlnThrPheTyrlaLeu 661
Db 2207 ACGGGC----- 2212
QY 662 SerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSeraspLysAla 681
Db 2212 ----- 2212
QY 682 ValAlaIaIaThrasnThrIleAlaAsnGlnIleasnThrAlaProLysProAlaAlaPro 701
Db 2213 -----CAGAAAGAACTTCTGCGCGCCCGCGCGCGCC 2245
QY 702 ThrThrLeuGlnIleProPro-----ProLeuProAla 712
Db 2246 ---CCTGTCCAGTGTCCGCGCTCCACTCTCGGACGACAGCCAGCCGCG---CCAGGG 2301
QY 713 IleLysHisLeuProArg-----ProGluThr-----LeuHis-ProasnProAlaGln 728
Db 2302 CCAGGCGACTCCCGCGTGGGGGACGAGGCTCCCTGTGGCATCCCGCGCGCGCTGC 2361
QY 728 yLeuGlnGlnIleSerIleSeraspValThrThrCysLeuValAlaSerLysGluasnValGln 748
Db 2362 CCACGAGCGGTCTGCTGCTCCCTACGCGCGGGGCAACCGCGCATGGAGTCTCTGGC 2421
QY 748 nValAlaGlnSerAsnLeuThrLys-----AspArgSerMetArgLysSerPheaspPhe 766
Db 2422 GCAGGAGGAGACCCCGGCGTCCAGGCGCCCGCGAGGAGACCTCGCGGAGCAGC----- 2473
QY 766 tGlyGlyGluThrLeuLeuSerValCysProMetValProLysaspLeuGlyLysSerLe 786

Db 2474 -----GACACGTCCATCTCCATCCCGTCCGTGGACCAAGAGAGCTGGAGCGTTCCTT 2526
QY 786 uSerValGlnasnLeuIleArgSerThrGluGluLeuAsn 799
Db 2527 CAGCGGCTTCAGCATCTCCAGTCCAGAGAGAGACCTGGAT 2566

Search completed: January 11, 2003, 18:07:01
Job time : 374 secs



GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2003, 17:57:22 : Search time 1959 Seconds
(without alignments)

7341.293 Million cell updates/sec

Title: US-09-810-796-5

Perfect score: 4547
Sequence: 1 MKDVSGRGRVLNSAARG.....STCKAGESTDAISLPVKK 888

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ .p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US09810796/funat.10012003_085456_22818/app_query.fasta.1.1031
-DB-EST -OPMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -STRAT=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09810796.ecgn.1.1191.etunac.10012003_085456_22818 -MCPU=6 -ICPU=3
-NO_XLPY -NO_MMAL -LARGEDBURY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: em_estdb:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estlom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vtl:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1258.5 | 27.7 | 997 | 10 | BB609854 |
| 2 | 1099 | 24.2 | 658 | 10 | BE158938 |
| 3 | 1043.5 | 22.9 | 679 | 10 | BE647997 |
| 4 | 1024.5 | 22.5 | 632 | 10 | BE624101 |
| 5 | 989 | 21.8 | 584 | 10 | AM049888 |
| 6 | 925 | 20.3 | 574 | 12 | BC532543 |
| 7 | 907.5 | 20.0 | 570 | 13 | BI033850 |
| 8 | 902 | 19.8 | 547 | 13 | BI034993 |
| 9 | 892 | 19.6 | 914 | 12 | BF312386 |
| 10 | 864 | 19.0 | 908 | 12 | BF240146 |
| 11 | 854.5 | 18.8 | 920 | 12 | BF317072 |
| 12 | 835.5 | 18.4 | 634 | 9 | AT589812 |
| 13 | 834 | 18.3 | 1004 | 14 | BO219245 |
| 14 | 831 | 18.3 | 506 | 12 | BF959996 |
| 15 | 813 | 17.9 | 597 | 10 | BE260338 |
| 16 | 802.5 | 17.6 | 625 | 10 | BB666833 |
| 17 | 797 | 17.5 | 469 | 10 | BE103175 |
| 18 | 792 | 17.4 | 491 | 12 | BF959488 |
| 19 | 748 | 16.5 | 541 | 9 | AT968605 |
| 20 | 729.5 | 16.0 | 771 | 9 | AT517016 |
| 21 | 721 | 15.9 | 626 | 10 | BB635544 |
| 22 | 719.5 | 15.7 | 434 | 12 | BG73257 |
| 23 | 713 | 15.7 | 438 | 13 | BI290441 |
| 24 | 700 | 15.4 | 477 | 17 | A2443500 |
| 25 | 697.5 | 15.3 | 698 | 13 | BM640404 |
| 26 | 695 | 15.3 | 435 | 12 | BF943257 |
| 27 | 689 | 15.2 | 502 | 9 | AT189222 |
| 28 | 687.5 | 15.1 | 517 | 12 | BF954375 |
| 29 | 664 | 14.6 | 568 | 14 | BO339931 |
| 30 | 656.5 | 14.4 | 655 | 12 | BF432555 |
| 31 | 651 | 14.3 | 469 | 9 | AT864554 |
| 32 | 618.5 | 13.6 | 600 | 9 | AU141948 |
| 33 | 618 | 13.6 | 448 | 10 | BO285922 |
| 34 | 617.5 | 13.6 | 448 | 14 | AV838434 |
| 35 | 603 | 13.3 | 427 | 12 | BF523361 |
| 36 | 586.5 | 12.9 | 1082 | 17 | CNS041K3 |
| 37 | 585.5 | 12.9 | 679 | 10 | BE675840 |
| 38 | 584.5 | 12.9 | 1087 | 17 | CNS05CVN |
| 39 | 577 | 12.7 | 407 | 9 | AT871198 |
| 40 | 559 | 12.3 | 537 | 12 | BE703020 |
| 41 | 556 | 12.2 | 622 | 10 | BE257127 |
| 42 | 541.5 | 11.9 | 567 | 13 | BM253726 |
| 43 | 538.5 | 11.8 | 846 | 13 | BI818397 |
| 44 | 535 | 11.8 | 671 | 10 | BB617583 |
| 45 | 534.5 | 11.8 | 535 | 12 | BF798694 |

ALIGNMENTS

RESULT 1
BB609854
LOCUS
DEFINITION
BB609854
ACCESSION
BB609854
VERSION
BB609854.1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

997 bp mRNA linear EST 31-AUG-2001
CDNA clone 1200002P22 5', mRNA sequence.
GI:15390457

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 997)
Arakawa, T., Carlini, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda

TITLE
JOURNAL
COMMENT

'M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Atakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka, T., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Atakawa, T., Ishii, Y. and Hayashizaki, Y.
Mapping of 1003 mouse cDNAs on mouse chromosomes. J. Struct. Funct. Genomics 2 pre, 172-186 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES
source

Location/Qualifiers
1. 997
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="1200002P22"
/clone_11b="RIKEN full-length enriched, adult male lung"
/sex="male"
/tissue_type="lung"
/dev_stage="adult"
/lab_host="SOLAR"
/note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']
GAGGAGAGACGGCGGCACTGAGATTGTTTGTGTTTNN 3'], cDNA was prepared by using trihalose reverse-transcribed reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5']
GAGGAGAGAGGATCCAGCGTCATTTATTTAAACCCCCCCCC 3'].
cDNA was cleaved with XhoI and SstI."
BASE COUNT 172 a 285 c 290 g 248 t 2 others
ORIGIN

Alignment Scores:

Pred. No.: 2,75e-121 Length: 997
Score: 1258.50 Matches: 237
Percent Similarity: 87.428 Conservative: 27
Best Local Similarity: 78.488 Mismatches: 33

Query Match: 27.68% Indels: 5
DB: 10 Gaps: 2
US-09-810-796-5 (1-888) x BB609854 (1-997)

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QY 112 SerThrIleProGluHisThrLysLeuAlaSerCysLeuIleIleGlnPheVal 131
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DB 156 TCCACCATCCAGAGACACAGAACTTCCCAACGAGTCTTCTTATCTTGGAATTCGTG 215
QY 132 MetIleValAlaPheGlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCys 151
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QY 152 ArgTYRArgGlyTyrPngInGlyArgLeuArgPheAlaArgGlyProPheCysValIle 171
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QY 172 ThrIleValLeuIleAlaSerIleAlaValAlaSerAlaTyrPngInGlyAsnIlePhe 191
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DB 396 GCTACGCGCGCTTGGCGAGATGCGCTTCTCATAGATCTCGCGAGCGCGATGAT 455
QY 212 ArgArgGlyLeuThrTyrPlyLeuGlySerValAlaTyrAlaHisSerIysGluLeu 231
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DB 456 CGCGCGGTGGACACTGGAAGCTGTGGATCGCTGATCGGACAGATAGAGACTG 515
QY 232 IleThrIleTyrIleGlyPheLeuValLeuIlePheSerPheLeuValTyrLeu 251
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DB 516 ATCACCGCTGCTGATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 575
QY 252 ValGluLysAspAlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTyrPngIle 271
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QY 272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTyrPngIleArg 291
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QY 292 LeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIle 311
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QY 367 ThrCys 368
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DB 936 TCTTGT 941

RESULT 2 BE158938 658 bp mRNA linear EST 21-JUN-2000
LOCUS BE158938
DEFINITION MRO-HT0404-210200-001-c04 HT0404 Homo sapiens CDNA, mRNA sequence.

ACCESSION BE158938
 VERSION BE158938.1 GI:8621659
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 638)
 Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.V.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-MR0-HM0404-210>)
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 High quality sequence stop: 657.
 Location/Qualifiers
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 /dev_stage="Adult"
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 BASE COUNT 181 a 175 c 153 g 149 t
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 Score: 1099.00 Matches: 211
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 Best Local Similarity: 99.06% Mismatches: 0
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 Gaps: 0
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 US-09-810-796-5 (1-888) x BE158938 (1-658)
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 QY 418 GlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLysSer 437
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 Db 438 CAGAGAGCTGGAGCTTCAACGACCCAGACCCGCTTCGGCGCTCGCTCCCAAAAGT 497
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 QY 438 SerGlnProLysProValIleAspAlaAspThrAlaLeuGlnLysThrAspValTrpAsp 457
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 QY 478 IleArgAlaIleArgIleMetLysPheHisValAlaLys 490
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 Db 618 ATTCGACCTATCGAATTTGAATTTCTTGTCCCAA 656
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 RESULT 3
 BE647997 679 bp mRNA linear EST 06-SEP-2000
 LOCUS UI-M-BH1-anr-g-09-0-UI.r1 NIH_BMAP_M.S2 Mus musculus cDNA clone
 DEFINITION UI-M-BH1-anr-g-09-0-UI 5', mRNA sequence.
 ACCESSION BE647997
 VERSION BE647997.1 GI:9973817
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 679)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 CONTACT: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mbest@mail.nih.gov
 cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
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 Location/Qualifiers
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 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The NIH_BMAP_M.S2 library is a subtracted library derived from

transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter or sequence [5': GAGGAGACATTCGTGGATTAAATTAATATCCCCCCCCCC 3'] cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KSI(+) after bulk excision from lambda FLIC I. Cloning sites, 5' end: SalI; 3' end: BamHI".

| | | | | |
|------------------------|----------|-------|---------------|-------|
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| Alignment Scores: | | | | |
| Pred. No.: | 5.53e-97 | | | |
| Score: | 1024.50 | | | |
| Percent Similarity: | 95.24% | | | |
| Best local Similarity: | 94.76% | | | |
| Query Match: | 22.53% | | | |
| DB: | 10 | | | |
| | | | Gaps: | 1 |
| | | | Mismatches: | 1 |
| | | | Conservative: | 19 |
| | | | Matches: | 632 |
| | | | Length: | 632 |

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| Db | 3 | AAGCTTTTGGAAAAGAGACACCAGCTGCCAACCCTCATCAGTGTGTCTGGCGTACT | 62 |
| QY | 346 | TyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysProHisLeuysAlaLeu | 365 |
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| QY | 366 | HisThrCysSerProThr-----AsnGlnLysLeuSer | 376 |
| Db | 123 | CACACCTCCACGCCCTTACCACAGAAAGACAGGAGGCATCAAGCAGTCAGAGGCTGAGAC | 182 |
| QY | 377 | PhelySGluAcGValArGMeAlaSerProArGgLYgInSerIleLysSerArGglnAla | 396 |
| Db | 183 | TTTAAAGAGACGAGTCCGATGGCTTAGCCCAAGGGCCAGAGCATTTAAGGACAGACAGCA | 242 |
| QY | 397 | SerValGlyAspArgArGSerProSerThrAspIleThrAlaGluGlySerProThrLys | 416 |
| Db | 243 | TCAGTAGCGTGAAGAGATCCCGGACACTGCATCAGTACGCGGAGAGGAGCCCAACAA | 302 |
| QY | 417 | ValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLys | 436 |
| Db | 303 | GTCCGGAAGAGTGGAGCGCTTCACACCCGAAACCCGCTTCAGGCGCTTCATACGCGCTCAAG | 362 |
| QY | 437 | SerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyr | 456 |
| Db | 363 | AGTTCCACGCCCAAAACCGAGTGAATGAACCCGACACAGCCCTTGGGATTCATGATGTGTAT | 422 |
| QY | 457 | AspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThr | 476 |
| Db | 423 | GATGGAAAGAGATGCCAGTGTACCTCTCTGTGGAGAGACTTACCACCATTTAAAC | 482 |
| QY | 477 | ValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThr | 496 |
| Db | 483 | GTCATCCGACGACATCAGATTATGCAAGTTTCATGTTGCAAAACCGGAAGCTTTAAAGAAACA | 542 |
| QY | 497 | LeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMet | 516 |
| Db | 543 | TTACGCCCATATGATGATAAAGATTCATGTAACATACCTGTGCTGGTGCACCTGGACATG | 602 |
| QY | 517 | LeuCysArgIleLysSerLeuGlnThrArg | 526 |
| Db | 603 | CTTTGTAGCATATAAAGCCTTCAGACACGC | 632 |

RESULT 5

AM049888

LOCUS

DEFINITION

UI-M-BHL-ent-r-g-09-0-UI s1 NIH BM4P M.S2 Mus musculus CDNA clone

UI-M-BHL-ent-r-g-09-0-UI 3', mRNA sequence.

AM049888

VERSION

AM049888.1 GI:5910417

584 bp

mRNA

linear

EST 18-SEP-1999

| KEYWORDS | EST. |
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| SOURCE | house mouse. |
| ORGANISM | Mus musculus |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus |
| AUTHORS | 1 (bases 1 to 584) |
| TITLE | Bonaldo,M.F., Lennon,G. and Soares,M.B. |
| JOURNAL | Normalization and subtraction: two approaches to facilitate gene |
| MEDLINE | discovery |
| COMMENT | Genome Res. 6 (9), 791-806 (1996) |
| | 97044477 |
| | Contact: Chin, H |

FEATURES
SOURCE

Location/Qualifiers

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/clone="UI-M-BH1-anr-g-09-0-UI"
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/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S2 library is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_LIB=NIH_BMAP_M_S2
TAG_TISSUE=corpus-striatum
TAG_SEQ=ACCGC"
107 a 151 c 174 g 152 t
BASE COUNT
ORIGIN

```

| | | | | | |
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| Alignment Scores: | | | | | |
| Pred. No.: | 2,656-93 | Length: | 584 | | |
| Score: | 989.00 | Matches: | 192 | | |
| Percent Similarity: | 99.48% | Conservative: | 1 | | |
| Best Local Similarity: | 98.97% | Mismatches: | 1 | | |
| Query Match: | 21.75% | Indels: | 0 | | |
| DB: | 10 | Gaps: | 0 | | |
| US-09-810-796-5 (1-888) x AM049888 (1-584) | | | | | |
| Oy | 17 | AAlaAaArGgLyAsPcLyLeuLeuLeuLeuLcUlyThrArgAlaAlaIatPhrLeuGlyGly | 36 | | |
| bDb | 3 | GCcGCGCAAGGGcGcAGcGcCTCtGTTCtCGcACCCcGcGcGcGcTTCgGcGAAGc | 62 | | |
| Oy | 37 | GlyGlyGlyLeuAuRgUsErFArgArgLyLySgInGlyAlaArMeSeTrLeuLeuGly | 56 | | |
| bDb | 63 | GCcGCGcGcCTTGAGAGAAGcGcGcGcGcCAAGcAGGcGcGcCcCAATATAGcCTTCcTGcGc | 120 | | |

| DB: | 13 | Gaps: | 0 |
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| US-09-810-796-5 (1-888) x BI034993 (1-547) | | | |
| QY 424 | AsnAspArgrThrArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProVal | 443 | |
| Db 3 | AAGGACCGAAGCCGGCTCCGGCCCTCGCTCGCTCAAAAGTTCTCAGCCAAACCAAGTGC | 62 | |
| QY 444 | ILAspAlaAspThrAlaLeuGlyThrAspAspAlaTyrAspGlyLysGlyCysGlnCys | 463 | |
| Db 63 | ATGATGCTGACAGCCCTTGGCAGCTGATGATATATATGATAAAGATGCGCAGTGT | 122 | |
| QY 464 | AspValSerValGluAspLeuThrProProLeuLysThrValIleArgAlaIleArgIle | 483 | |
| Db 123 | GATGATCAGTGAAGAACCTCACCCCACTTAAACTGATTCATTCAGAGTATCAGAAATT | 182 | |
| QY 484 | MetLysPheHisValAlaLysArgLysPheLysGlyIleuThrLeuArgProTyrAspValLys | 503 | |
| Db 183 | ATGAAATTCCTGTTGCAAAACGGAAGTTTAAAGAAACATTACGTCCTATGATGATTA | 242 | |
| QY 504 | AspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuLysArgIleLysSerLeu | 523 | |
| Db 243 | GATGTCATTGAAACAATATTCTGCTGATCATCTGGAACATGTTGTGAGAAATTAAGCCTT | 302 | |
| QY 524 | GlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArg | 543 | |
| Db 303 | CAAAACAGCTGTGATCAAAATCTTGGAAGGGAACACATCAGATGAAGAAGGCCGA | 362 | |
| QY 544 | GluLysIleThrAlaGluHisGlyIleThrThrAspAspLeuSerMetLeuGlyArgValAl | 563 | |
| Db 363 | GAGAAATATACAGACAGAACATGAGACCCACACACATCTCAATATGCTCAGTGGGTGTC | 422 | |
| QY 564 | LysValGlyLysGlnValGlnSerIleGlnSerLysLeuAspCysLeuLeuAspIleTyr | 583 | |
| Db 423 | AAGCTTGAAGAAACAGGTACGTCATGAAATCCAAAGCTGGAGCTGCTACTGACATTCAT | 482 | |
| QY 584 | GlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIlePro | 603 | |
| Db 483 | CAACAAGCTCTTCGGAAGGCTGTGCTCAGCCCTCGCTGTTGTTCAATCCAGATCCCA | 542 | |
| QY 604 | Pro 604 | | |
| Db 543 | CCT 545 | | |
| RESULT 9 | | | |
| LOCUS | BF312386 | | |
| DEFINITION | 6018989926F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127958 5', | | |
| ACCESSION | BF312386 | | |
| VERSION | BF312386.1 | | |
| KEYWORDS | EST. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | |
| TITLE | 1 (bases 1 to 914) | | |
| JOURNAL | NIH-MGC http://mgc.nci.nih.gov/. | | |
| COMMENT | National Institutes of Health, Mammalian Gene Collection (MGC) | | |
| | unpublished (1999) | | |
| | Contact: Robert Stransberg, Ph.D. | | |
| | Email: cgapbs-remail.nih.gov | | |
| | Tissue Procurement: ATCC | | |
| | cDNA Library Preparation: Ling Hong/Rubin Laboratory | | |
| | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) | | |
| | DNA Sequencing by: Incyte Genomics, Inc. | | |
| | Clone distribution: MGC clone distribution information can be | | |
| | found through the I.M.A.G.E. Consortium/LNLN at: image.jnl.gov | | |
| | Plate: L1CMI020 row: d column: 07 | | |
| | High quality sequence stop: 630. | | |
| FEATURES | Location/Qualifiers | | |
| SOURCE | 1..914 | | |
| | /organism="Homo sapiens" | | |

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| DB | 294 | 3133 | 65.81% | 18 | 12 |
| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | 76.84% | 30 | 46 |
| DB | 294 | 3133 | 65.81% | 18 | 12 |
| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | 76.84% | 30 | 46 |
| DB | 294 | 3133 | 65.81% | 18 | 12 |
| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | 76.84% | 30 | 46 |
| DB | 294 | 3133 | 65.81% | 18 | 12 |
| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | 76.84% | 30 | 46 |
| DB | 294 | 3133 | 65.81% | 18 | 12 |
| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | 76.84% | 30 | 46 |
| DB | 294 | 3133 | 65.81% | 18 | 12 |
| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | 76.84% | 30 | 46 |
| DB | 294 | 3133 | 65.81% | 18 | 12 |
| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | 76.84% | 30 | 46 |
| DB | 294 | 3133 | 65.81% | 18 | 12 |
| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | 76.84% | 30 | 46 |
| DB | 294 | 3133 | 65.81% | 18 | 12 |
| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | 76.84% | 30 | 46 |
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| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | 76.84% | 30 | 46 |
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| DB | 294 | 3133 | 65.81% | 18 | 12 |
| DB | 278 | 2933 | 19.62% | 4 | 12 |
| DB | 601 | 6588 | | | |

QY 314 GlyPheAlaLeuIysValGlnGlnGlnHisArgGlnIleHisPheGlnIleValArgAsn 333
 ||||| : : : : :
 Db 701 GGGTTGGC---CCGTTAAGTCCAGAGACGAGCGGAACCTGGGAGAGGGGAACCCGG 757
 QY 334 ProAlaAlaAsnLeuIleGlnCysValTrpArgSer 345
 : : : : :
 Db 758 AAGCGTTCA-----TGGCGGAGCT 775
 RESULT 10
 BF240146 908 bp mRNA linear EST 14-NOV-2000
 LOCUS 601905649P1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133293 5',
 DEFINITION mRNA sequence.
 ACCESSION BF240146
 VERSION BF240146
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 908)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LNCM1034 row: b column: 14
 High quality sequence stop: 615.
 Location/Qualifiers
 1..908
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4133293"
 /clone_1lb="NIH_MGC_54"
 /tissue_type="from chronic myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
 Site_1: SfiI (ggcgccgcgcgc); Site_2: SfiI (ggccatagccg
); Double-stranded cDNA was prepared from cell line RNA.
 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCGCATTTGCGC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCGAGCGCGCCGACATG-3' (30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 clones
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."
 BASE COUNT 263 a 229 c 217 g 199 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 7,49e-80 Length: 908
 Score: 864.00 Matches: 205
 Percent Similarity: 90.95% Conservative: 6
 Best Local Similarity: 88.36% Mismatches: 11
 Query Match: 19,00% Indels: 12
 DB: 12 Gaps: 0
 US-09-810-796-5 (1-888) x BF240146 (1-908)
 QY 667 SerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsn 686
 ||||| : : : : :
 Db 2 AGTCAAGCAACACAGGTCGCAATTAGTCAAGGATGCTCAGACGTGCGACGCCACCAAC 61
 QY 687 ThrIleAlaAsnGlnIleAsnThrAlaProIysProAlaIleAlaProThrTrpIleGlnIle 706

Db 62 ACCATTGCACCAACCAATTAATACGGACCCAGACAGCCCAACCAACTTACGATC 121
 QY 707 ProProIleuProAlaIleIleHisIleuProArgProGluThrIleHisProAsnPro 726
 ||||| : : : : :
 Db 122 CCACCTCCCTCCGCCACCATCAAGCATCTGCCAGGCA-GAAACTGTGACCTTAACCT 180
 QY 727 AlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerIysGluAsn 746
 ||||| : : : : :
 Db 181 GCAGGCTTACAGAAAGCATTTCTGACGTCCACCACCTGCTTGTGCTCCCAAGGAAAT 240
 QY 747 ValGlnValAlaGlnSerAsnLeuThrIleHisArgSerMetArgIysSerPheAspMet 766
 ||||| : : : : :
 Db 241 GTTCAAGTTGCACAGTCAATATCTCACCAAGACCGTTCTATGAGAAAGCTTTGACATG 300
 QY 767 GlyGlyGluThrLeuLeuSerValCysProMetValProllysAspLeuGlyIysSerLeu 786
 ||||| : : : : :
 Db 301 GGAGGAGAAACTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 360
 QY 787 SerValGlnAsnLeuIleArgSerThrGlnGluLeuAsnIleGlnLeuSerGlySerGlu 806
 ||||| : : : : :
 Db 361 TCTGTGCAAAACCTGATCAGTGCAGCCGAGAACTGAATATCAACTTTCAGGAGACTGAG 420
 QY 807 SerSerGlySerArgGlySerGlnAspPheTyrrProIysTrpArgGluSerIysLeu--P 826
 ||||| : : : : :
 Db 421 TCAAGTGGCTCCAGAGGCGAG-CAGATTTTTCACCCCAATGAGGGAATCCAAATGCTT 479
 QY 826 IleIleThrAspGluGluValGly--ProGlnGluThrGlnThrAsp-ThrPheAspAla 845
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 Db 480 TTATTAAGTATGATGAAGAGGAGGAGTCCCGAAGAGAGACAGACAGACACTTTGATGCCG 539
 QY 845 IapGlnIleProIleArgGlnAlaIlePheAlaSerAspSerLeuArgThrGlyArgSer 864
 ||||| : : : : :
 Db 540 CACGAGTCTCCCGGGGAAAGCTGCTTTGATGATGATGATGATGATGATGATGATGATGATG 599
 QY 865 ArgSerSerGlnSerIle-CysIysAla-GlyGluSer-ThrAspAlaLeuSer-IleuP 883
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 Db 600 CGATCATCTCAGACGATTTTGTAAAGCCAGAGACAGATACGATGATGATGATGATGATGATG 659
 QY 883 CHisAlaIysLeuIys 888
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 Db 660 TCATGTCAAACTTGAA 675
 RESULT 11
 BF317072 920 bp mRNA linear EST 21-NOV-2000
 LOCUS 601903470P1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136200 5',
 DEFINITION mRNA sequence.
 ACCESSION BF317072
 VERSION BF317072
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 920)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at: image.llnl.gov
 Plate: LNCM1041 row: k column: 17
 High quality sequence stop: 714.
 Location/Qualifiers
 1..920
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 /db_xref="taxon:9606"

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| | | /clone="IMAGE:4136200" | |
| | | /tissue_type="neuroblastoma" | |
| | | /lab_host="DH10B (phage-resistant)" | |
| | | /note="Organ: brain; Vector: pORF7; Site_1: XhoI; Site_2: | |
| | | EcoRI; CDNA made by oligo-dT priming. Directionally | |
| | | cloned into EcoRI/XhoI sites using the following 5' | |
| | | adaptor: GGCACGAG(G). Library constructed by Ling Hong | |
| | | in the laboratory of Gerald M. Rubin (University of | |
| | | California, Berkeley) using ZAP-CDNA synthesis kit | |
| | | (Stratagene) and Superscript II RT (Life Technologies). | |
| | | Note: this is a NIH-MGC library." | |
| BASE COUNT | 150 a | 256 c | 298 g 216 t |
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| Alignment Scores: | 7,64e-79 | Length: | 920 |
| Pred. No.: | 854.50 | Matches: | 184 |
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| Percent Similarity: | 68.91% | Mismatches: | 55 |
| Best local Similarity: | 18.79% | Indels: | 9 |
| Query Match: | 12 | Gaps: | 3 |
| D8: | | | |
| US-09-810-796-5 (1-888) x BF317072 (1-920) | | | |
| Oy | 78 AsnTyRLeuTyRAsnValLeuGIuArgProArggLyTrpAlaPheLleTyRHISAlaPhe | 97 | |
| | | | |
| Db | 1 GATTTCCTCTACACCGTGCGGAGCGGGC-CGGCGCTGGGGCTTCATCCACCCTCAC | 59 | |
| Oy | 98 -ValPheLeuLeuValPheGlYcysLeuIlleLeuSerValPheSerThrIleProGUHt | 117 | |
| | | | |
| Db | 60 GGTTGTTCCTCTGGTTTTCTCTCGGCCCTCGTCTCTGTGTTTCCACCATCAAGAGTA | 119 | |
| Oy | 117 sPhrILsLeuAlaSerSercYsLeuLeuIlleLeuGIuPheValMetIleValValPheGl | 137 | |
| | | | |
| Db | 120 TCAGAGAAGACTCGGAGGGGGCCCTCTACATCCCTGGAATCGTAGATACGTGCTT-GG | 178 | |
| Oy | 137 yLeuGIuPheIleIleArgIleTrpSerAlaGlYcysCysArGYrARGLYTTPel | 157 | |
| | | | |
| Db | 179 CGTGAGTACTTCGTGGGCGATCTGGGGCGCGCGCTGCTGCTGCGGTACCGGTGGAG | 238 | |
| Oy | 157 nGIyArGLeuArgPheAlaArgLysProPheCysValIleAspThrlIleValLeuIleA | 177 | |
| | | | |
| Db | 239 GGGCGCGCTCAAGTTGGCCCGAAACGGTTGTGTGATGATACATCATGCTCATCGC | 298 | |
| Oy | 177 aserIleAlaValSerAlaLysTrhINGlYAsnIlePhealThrSerAlaLeuAr | 197 | |
| | | | |
| Db | 299 CTCGATTGGCGTCTGGCCCCGGCGCTCCAGGACAAGCTCTTTGGCACATCTGGCGTCG | 358 | |
| Oy | 197 gSerLeuArgPheLeuGIuIlleLeuArgMetValArgMetLspArgAglyLYThrr | 217 | |
| | | | |
| Db | 359 GAGCCCTCGCTTCCTCGAGATTCTGCGGATATCCGCAATGACCGCGGGAGGACCGT | 418 | |
| Oy | 217 PLSyLeuLeuGLYSerValValYrAlaHisSerLySGluLeuIleThAlaTrpTYrtI | 237 | |
| | | | |
| Db | 419 GAAGCTGCTGGGCTCTGTGTGTATGCCCACAGCAGGAAGCTGTGACACTGTGGTACAT | 478 | |
| Oy | 237 eglYrPheLeuValLeuIlePheSerSerPheLeuValYrLeuValGIuLysASPAlas | 257 | |
| | | | |
| Db | 479 CGGCTTCCTTGTGCTCATCCCGGCTCGTCTGTGTACTGTGAGAGAGAACGGGAGAA | 538 | |
| Oy | 257 nLysGIuPheSerThrYrAlaAspAlaLeuTrpPrpGLyThrlIethLeuThrrILI | 277 | |
| | | | |
| Db | 539 CGA-CACATTGGACACCTACGCGGATGACTGTGTGGGGCCGTGATCACCCTGACAT-- | 595 | |
| Oy | 277 eglYrYrGIASpLysThrProLeuThTrPLeuGIuYrGLeuLeuSerAlaGIyPheAl | 297 | |
| | | | |
| Db | 596 -TGGTACGGGAGACAAGTACCCACAGACTCGGAACGAGAGTC-CTTGGCGAACCTTCACC | 653 | |
| Oy | 297 aleuLeuGIILeserPhePheAlaLeuProAlaGIYLileuGIySerGIyPheAlaLe | 317 | |
| | | | |
| Db | 654 CTCATGCGGTGTCTCCCTTCTCCGCGCTGCGAGGACATCTTGGGGGTGTGGTTGGCCT | 713 | |

| | | | |
|------------------------|---|---|-----|
| OY | 317 | utysvalGInGlncInGlnHhSArGGLnLysSHSISPhEgLuLusArGrArGsNPrOxlaAlAAs | 337 |
| Db | 714 | GAACTTCAGGGAGCGACGCAGGCCAGCAACTTG-----AGAAAGAGGGGAACCGGAGGA | 767 |
| OY | 337 | nleuIlEGlncYsValTTP | 343 |
| Db | 768 | GGCTGATCAGTGTG---TTGG | 783 |
| RESULT 12 | | | |
| LOCUS | A1589812 | | |
| DEFINITION | A1589812 | 634 bp mRNA linear EST 12-MAY-1999 | |
| ACCESSION | U074F08.x1 NCI-CGAP-Brn25 Homo sapiens cDNA clone IMAGE:2163879 | | |
| VERSION | A1589812 | similar to TR:099454 Q99454 HNSPC.; mRNA sequence. | |
| KEYWORDS | A1589812.1 GI:4598860 | | |
| SOURCE | EST. | | |
| ORGANISM | human. | | |
| REFERENCE | Homo sapiens | | |
| AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| TITLE | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| JOURNAL | NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. | | |
| COMMENT | 1 (bases 1 to 634) | | |
| | National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTAGP), Tumor Gene Index | | |
| | Unpublished (1998) | | |
| | Contact: Robert Strausberg, Ph.D. | | |
| | Email: rgsaps@remail.nih.gov | | |
| | Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfield M.D., Ph.D. | | |
| | cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. | | |
| | cDNA Library Arrayed by: Greg Lennon, Ph.D. | | |
| | DNA Sequencing by: Washington University Genome Sequencing Center | | |
| | clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: | | |
| | www.bio.linnl.gov/btbp/Image/image.html | | |
| | Insert Length: 1063 Std Error: 0.00 | | |
| | Seq primer: -40UP from Glibco | | |
| | High quality sequence stop: 457 | | |
| POLYA=NO. | | | |
| FEATURES | | | |
| SOURCE | | | |
| | Location/Qualifiers | | |
| | 1..634 | | |
| | /organism="Homo saplens" | | |
| | /db_xref="taxon:9606" | | |
| | /clone="IMAGE:2163879" | | |
| | /clone_lib="NCI-CGAP_Brn25" | | |
| | /tissue_type="anaplastic oligodendroglioma" | | |
| | /lab_host="TDH10B" | | |
| | /note="Organ: brain; Vector: pRT73D-Pac (Pharmacia) with e modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCATCTGTAAGTGGAGCGCCGCAATAGGTTTTTTTTTTTTTTT T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library is normalized, and was constructed by Benco Soares and M.Fatima Bonaldo." | | |
| BASE COUNT | 99 a 190 c 187 g 154 t | 4 others | |
| ORIGIN | | | |
| Alignment Scores: | | | |
| Pred. No.: | 4,24e-77 | Length: | 634 |
| Score: | 835.50 | Matches: | 158 |
| Percent Similarity: | 85.56% | Conservative: | 20 |
| Best Local Similarity: | 75.96% | Mismatches: | 30 |
| Query Match: | 18.37% | Indels: | 1 |
| DB: | 9 | Gaps: | 0 |
| OS | -09-810-796-5 (1-888) x A1589812 (1-634) | | |
| OY | 89 | GI:YTTPAlaPheTLeYrThIsAlaPheVaIPHeLeuValIPHeIGlycSeuIleLeu | 108 |

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 QY 109 SerValPheSerThrIleProGluHisThrLysLeuAlaSerSerLysLeuIleLeu 128
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 VERSION BQ219245.1 GI:20400645
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1004)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
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 /note="Organ: pancreas; Vector: pCMV-Sport6; Site_1: NotI;
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 Average insert size 1.1 kb. Library constructed by Life
 Technologies."

BASE COUNT 201 a 323 c 263 g 216 t 1 others
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 Score: 834.00 Matches: 180
 Percent Similarity: 67.68% Conservative: 21
 Best Local Similarity: 60.61% Mismatches: 65
 Query Match: 18.34% Indels: 31
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US-09-810-796-5 (1-888) x BQ219245 (1-1004)

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| JOURNAL | Contact: Simpson A.J.G. | | |
| MEDLINE | Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV2&t2-QV2-NN0045- 051200-526-909&t3=2000-12-05&t4=1) Seq primer: puc 18 forward High quality sequence stop: 506. | | |
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| BASE COUNT | | | |
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| QY | 492 | LysPheLysGluThrLeuArgProTyrAspValLysAspVal11leGluLInPyrSerAla | 511 |
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| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| REFERENCE | 1 (bases 1 to 597) | | |
| AUTHORS | NIH-MGC http://mgc.nci.nih.gov/. | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | |
| JOURNAL | Unpublished (1999) | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. Email: cgapbs-rt@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LHCMI87 row: j column: 02 High quality sequence stop: 597. | | |
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| | /lab_host="DH10B (phage-resistant)" | | |
| | /note="Organ: brain; Vector: pOTB; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit | | |

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: January 11, 2003, 17:58:52 ; Search time 65 Seconds
(without alignments)
4189.676 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MDVSGRGRLNSAARG.....SICKAGESTDLSPHYKUK 888

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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| 26 | 901.5 | 19.8 | 866 | 4 | US-09-105-058C-1 | Sequence 3, Appl |
| 27 | 260.5 | 3.7 | 1927 | 4 | US-09-336-643A-3 | Sequence 9, Appl |
| 28 | 250 | 3.5 | 3424 | 4 | US-09-336-643A-9 | Sequence 5, Appl |
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| 31 | 243 | 5.3 | 2064 | 4 | US-09-178-109-3 | Sequence 1, Appl |
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| 38 | 224 | 4.9 | 3102 | 4 | US-09-336-643A-7 | Sequence 17, Appl |
| 39 | 217.5 | 4.8 | 2483 | 1 | US-08-464-340A-3 | Sequence 3, Appl |
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| 41 | 215 | 4.7 | 649 | 4 | US-09-177-650-118 | Sequence 118, App |
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| 44 | 214 | 4.7 | 696 | 1 | US-07-955-916-5 | Sequence 5, Appl |
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ALIGNMENTS

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Sequence 95, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCMQ2 AND KCMQ3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09177, 650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 95
LENGTH: 3237
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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US-09-177-650-95
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Score: 1794.00
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Best Local Similarity: 45.14%
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Db 779 TCGAAGCTCTGGGCTCTGTGCTATGCCACACAGAGAGTGTGCTGCTGCTG 838
QY 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGlnLysAspAla 256
Db 839 ATCGGCTTCTGTTGCTCATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 898
QY 257 AsnLysGlnPheSerThrTyrAlaAspAlaLeuTyrPheGlyThrIleThrLeuThr 276
Db 899 AAGCAGCACTTGGACACCTACCGCGATGCTGTGTGGGCTGTGCTGCTGCTGCTG 958
QY 277 IleGlyTyrGlyAspLysThrProLeuThrTyrPheGlyArgLeuLeuSerAlaGlyPhe 296
Db 959 ATTTGCTAGCGGAGCAAGACCCCGACCTGGAACGGAGCTCTCTGCGCAACCTTC 1018
QY 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
Db 1019 ACCCTCATCGGTGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1078
QY 317 LeuLysValGlnGlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAla 336
Db 1079 CTGAAGGTTTCAGGAGACACAGGAGAGACTTTGAGAAAGAGCGGAGAACCGGACGA 1138
QY 337 AsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAsp----- 349
Db 1139 GGCCTGATCGAGTGGCGCTGAGATTTACGCAACACCTCTGCGCAGACACTGAC 1198
QY 350 -----GlnLysSerValSerIleAlaThrTyrLys----- 359
Db 1199 TCACAGTGGCAGTCTACGAGGAGGAGTCCGCTCCTGCTGCTGCTGCTGCTGCTGCTG 1258

QY 360 -----ProHisLeuLysAlaLeuHisThr----- 367
Db 1259 ACCCTACGGGCGCTCCAGACTTATCCCGCGCGGAGAACAGCTGTGAGAACCTC 1318
QY 367 ----- 367
Db 1319 AAGACTAAATCTGACGCTGCTTTCAGGAAGACCCCGCGCGAGCCGCTCCAGTAA 1378
QY 368 -----CysSerPro-----ThrAsnGlnLysLeu 375
Db 1379 GGCAGCCCGCTGCAGAGGCGCCCTGTGTGATGCTGCCCCGAGCGCTTACGCAAGAGT 1438
QY 376 SerPheLysGlnArgValArgMetAlaSerProArgGlnGlnSerIleLysSerArgGln 395
Db 1439 ACTTGAAGATCGTGTCTCTCCAGCCCGAGCGCTGCTGCTGCTGCTGCTGCTGCTG 1495
QY 396 AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGlySer 413
Db 1496 TCCCGCGAGCGCCAGACTGTGAGCGGTCACCGCCAGCCGAGAGCTTGAAGAGAGC 1555
QY 414 ProThrLysValGlnLysSerTyrSerPheAsnSparArgThrArgPheArgProSerLeu 433
Db 1556 CCCAGCAAGAGTGCACAGAGCTTGAGCTTGGGAGCGGAGCGGAGCGGAGCGGAGCTTTC 1615
QY 434 ArgLeuLysSerSerGlnProLysProValIleAspAlaSerThrAlaLeuGlyThrAsp 453
Db 1616 CCGATCAAGGCTGCGCGCTACGCGCAGAGCTCAGAA-----CAAGCAACCTCCCGGAGAG 1672
QY 454 AspValTyrAspGlnLysGlyGlnCysAspValSerValGlnAspLeuThrProPro 473
Db 1673 GACATGTGTGATGACAGAGCTGCGCGCTGCGAGTGTGTACCGAGGAGCTGACCCCGG 1732
QY 474 LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe 493
Db 1733 CTCAAACTCAGCATCAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1792
QY 494 LysGlnThrLeuArgProTyrAspValLysAspValIleGlnGlnTyrSerAlaGlyHis 513
Db 1793 AAGAGAGCGCTGCGCGCGCTTACGAGCTGATGACCTCATCTCAGAGTACTACCGCGG 1852
QY 514 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLys 533
Db 1853 CTGACATGCTGTCCGCAATTAGACCTGCTGACGTGACAGATGACAGATCGTGGGCG 1912
QY 534 GlyGlnIleThrSerSparLysSerArgGlyLysIleThrAlaGlnHisGlnThrThr 553
Db 1913 GCGCCAGCGATCAGGAC--AAGACCGCAGCAGCAAGGCGCGCGGAGGAGCTGCC 1969
QY 554 AspAspLeuSerMetLeuGlnArgValValLysValGlnLysGlnValGlnSerIleGln 573
Db 1970 GAGAGCCCGACGATGATGAGGAGCGCGGAGAGGTGAGAGACAGGCTTCTTCATGGAG 2029
QY 574 SerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaSer 593
Db 2030 AAGAACTGTGACTCTCTGTGATATCTACATCCAG-----CGATGGGC----- 2074
QY 594 AlaLeuAlaLeuAlaSerPheGlnIleProPheGlnLys----- 607
Db 2075 -----ATCCCGCGAGAGAGACCGGAGCGCTACTTTGGGCGC 2110
QY 608 -----GlnGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGly 624
Db 2111 AAGAGCCCGAGCGCGCGCGCTGACACACCGCGGAAAGAGAGCGGAG----- 2161
QY 625 SerAlaGlnAspSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeu 644
Db 2162 CATGTGACAGGAGCAGGCTGATTTGCAAGATCGCGCTCCAGCAGCTCCAGCGGC--- 2218
QY 645 GlnPheIleLeuThrProAsnGlnPheSerAlaGlnThrPheTyrAlaLeuSerProThr 664
Db 2218 ----- 2218
QY 665 MetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAla 684
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| Alignment Scores: | | | |
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| Pred. No.: | 4,34e-166 | Length: | 3287 |
| Score: | 1792.50 | Matches: | 411 |
| Percent Similarity: | 58.90% | Conservative: | 102 |
| Best Local Similarity: | 47.19% | Mismatches: | 181 |
| Query Match: | 39.42% | Indels: | 178 |
| DB: | 4 | Gaps: | 22 |
| US-09-810-796-5 (1-888) x US-09-105-058c-19 (1-3287) | | | |
| QY | 17 | AlaAlaIarqciLyaspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThleuGlyGly | 36 |
| DB | 160 | TCACACCCGAGGAGGGGGCCCTGCTGATGCGCGGCTCCGAGGCCCAAG-----CGC | 210 |
| QY | 37 | GlycylGlyLeuArgGlyuSerArgArgGlyLySGInGlyAlaArgMetSerLeuLeuGly | 56 |
| DB | 211 | GGGACATTCCTTCACAAACCTCCGCGGGGGGGGGGGGGCC-----GGG | 255 |
| QY | 57 | LysProLeuSerThrThrSerSerGlnSerCysArgArgAsnValLysThrArgArgVal | 76 |
| DB | 256 | AAGGCC-----CCCAAGCCCAAGGCCCTTCCTACCGCAACCTG | 291 |
| QY | 77 | GlnAsnThrLeuThrAsnValLeuGluArgProArgLyTPRAlaPheThrHisAla | 96 |
| DB | 292 | CAGAAATTCCTCTCAACAACGTGCGAGCGCGCGCGGCTGACCTTATACCAAGCC | 351 |
| QY | 97 | PheValPheLeuLeuValPheGlyCysLeuLileuSerValPheSerThrLeuProGlu | 116 |
| DB | 352 | TACGTGTCTCTCTGTTTCTTCTCTGCTCCGTGCTGTGTCTTCTTCCACCATCAAGAG | 411 |
| QY | 117 | HisThrLysLeuAlaSerSerCysLeuLeuLileuGluPheValMetLileValPhe | 136 |
| DB | 412 | TATGAGAGAGCGCTGGAGGGGGCCCTCTACATCCGGAACATCGCATATCGTGCTTT | 471 |
| QY | 137 | GlyLeuGluPhePheLleLeuArgLleThrSerAlaGlyCysCysArgTyArgGlyTTP | 156 |
| DB | 472 | GGCGTGGATGACTCGTGCGGATCTGGGGCCGACGCTGCTCTCCGTAACCATCAAGTCTG | 531 |
| QY | 157 | GlnGlyArgLeuArgPheAlaArgLysProPheCysValLleAspThrLileValLle | 176 |
| DB | 532 | AGGGGGGGGCTCAAGATTGGCCGGAAACCGTTCGTGTGATGATGATCATCATGATGCTCATC | 591 |
| QY | 177 | AlaSerLleAlaValValSerAlaLysThrGlnLysnLlePheAlaThrSerAlaLeu | 196 |
| DB | 592 | GCCTCATTTCCGCTGCTGGCCGGCCGCCAGGCAACCTTTTCCATCTCCATCTCGCTCC | 651 |
| QY | 197 | ArgSerLeuArgPheLeuGlnLileuArgMetValArgMetAspArgArgGlyGlyThr | 216 |
| DB | 652 | CGAGACCTGCGCTTCTCTCAGATTCTCGGATATCCGCATGACCGGGGGGAGGACAC | 711 |
| QY | 217 | TrpLysLeuLeuGlySerValValTyAlaHisSerLysLleuLleThrLleThrLleThr | 236 |
| DB | 712 | TGGAAAGCTGCTGGCTCTGTGTGTATGCCACAGCAAGAGAGCTGTGCTACCTCGTGTAC | 771 |
| QY | 237 | LleGlyPheLeuValLlePheSerSerPheLeuValTyLeuValGluLysAspAla | 256 |
| DB | 772 | ATCGGCTTCCTTGTCTCATCTCCGCTGCTGCTTCTGTGTACTGGACAGAAAGGGGAG | 831 |
| QY | 257 | AsnLysGluPheSerThrTyAlaAspAlaLeuThrTPRPolTyThrLleThrLeuThrThr | 276 |
| DB | 832 | AACGACCACTTTGACACCTACCGGGGATGCACTGTGTGGGGCTGATCACGCTGACACC | 891 |
| QY | 277 | LleGlyTyArgLysAspLysThrProLeuThrThrPheGlyArgLeuLeuSerAlaGlyPhe | 296 |
| DB | 892 | ATTGGCTTACGGGGAGCAGATGCCCAAGCTGACACGCGAGGCTCTTGGCGCAACCTTC | 951 |
| QY | 297 | AlaLeuLeuGlyLleSerPhePheAlaLeuProAlaGlyLleLeuGlySerGlyPheAla | 316 |
| DB | 952 | ACCTCATCGGTGTCTCTCTTCCGCTGCTCCGACGAGCATTTGGGCTTGGCTTTGCC | 1011 |
| QY | 317 | LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla | 336 |
| DB | 1012 | CTGAAAGTTTCAGGAGCAGCAGCAGCAAGCACTTTGGAAGAGGGCGAAACCCGGCAGCA | 1071 |

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QY 337 AsnLeu1leGlnCysValThrPargSerTyrAlaAlaasp----- 349
Db 1072 GGCCTGATCCAGTCGGCTGGAGATTTTACGCCCAACCTCTCCGCCACAGACTGCAC 1131
QY 350 -----GluLysSerValSer1leAlaThrTyrLys----- 359
Db 1132 TCCACGTGACACTACAGACGACGACGTCACGTCGCCCATGTACAGTTCGCAACTCA 1191
QY 360 -----ProHisLeuLysAlaLeuHisThr----- 367
Db 1192 ACCACGGGGCTCCAGACTATATCCCCCGCTGAACCAAGCTGAGCTCTGAGAAACCTC 1251
QY 367 ----- 367
Db 1252 AAGAGTAATCTGACTCGCTTTCAGAGAACGCCCGCCGCGAGCCCTCCAGTAA 1311
QY 368 -----CysSerPro-----ThrAsnGlnLysLeu 375
Db 1312 GGCAGCCCGTCAGAGGGCCCTGTGTGATGCTCCCCGAGCTGTAGCCAGAGAGTTC 1371
QY 376 SerPheLysGlnArgValArgMetLaserProArgGlyGlnSer1leLysSerArgGln 395
Db 1372 AGTTTGAAAGATCGTGC-----TTCCTCAAGCCCCCGAGCGCTGGCTCCCAAGGGAAGGG 1428
QY 396 AlaSerValGlyAsp-----ArgArgSerProSerThrAsp1leThrAlaGluLysSer 413
Db 1429 TCCCCCGAGCCCGACACTGTAGGGGGTCCACCAGCCGACAGAGCTTCGAGACAGC 1488
QY 414 ProThrLysValGlnLysSerThrSerPheAsnAspArgThrArgPheArgProSerLeu 433
Db 1489 CCCAGCAGAGCTGCCAAGAGCTGAGACTTGGGAGCCGACCGCGGACACCCAGGCTTTC 1548
QY 434 ArgLeuLysSerSerGlnProLysProVal1leAspAlaSerPheAlaLeuGlyThrAsp 453
Db 1549 CGCATTCAGAGGCTGGCGGCTCAGCGGC-----AACTCAGAACCAAGCCCTCCCGAGAG 1602
QY 454 AspValTyrAspGlnLysGlyCysGlnCysAspValSerValGlnLysLeuThrProPro 473
Db 1603 GACATTTGTGATGACACAAAGCTGCCCTCGAGTTTGTGACCAAGAGCTGAGACCCCGGC 1662
QY 474 LeuLysThrVal1leArgAla1leArg1leMetLysPheHisValAlaLysArgLysPhe 493
Db 1663 CTCCAAGTCAGATCAGAGCCGTGTGTATGCGGTTCTCTGTGTCCAAAGCGCAACTTC 1722
QY 494 LysGlnThrLeuArgProTyrAspValLysAspVal1leGluGlnTyrSerAlaGlyHis 513
Db 1723 AAGGAGAGCTGGCGGCTCAGACGTGATGAGCTCATCGAGCTACTCAGCGCGGCAC 1782
QY 514 LeuAspMetLeuLysArgLysSerLeuGlnThrArgValAspGln1leLeuGlyLys 533
Db 1783 CTCGACATGCTGCCGAATTAAGAGCTGTGATGCCAGAGTGGACACAGATGTGGGGGG 1842
QY 534 G1yG1n1leThrSerAspLysSerArgGlnLys1leThrAlaGlnHisGluThrThr 553
Db 1843 GGCCCGACGATCAGAGC-----AAGGACCGGACCAAGGGCCCGCGGAGCGGAGCTGCC 1899
QY 554 AspAspLeuSerMetLeuGlyArgValLysValLysGlnLysGlnValGlnSerLeu 573
Db 1900 GAGGAGCCCGCATGATGAGCGAGCTCGGAGAGTGGAGAGCAGAGCTTGTGCCATGGAG 1959
QY 574 SerLysLeuAspCysLeuLeuAsp1leTyrGlnGlnValLeuArgLysGlySerAlaSer 593
Db 1960 AAGAAAGCTGACTCTTGATTAATATCTACATGCAG-----CGGATGGCC----- 2004
QY 594 AlaLeuAlaLeuAlaSerPheGln1leProPheGluCys----- 607
Db 2005 -----ATCCCCCGACAGAGACAGAGCCGAGGCTTGTGGGCC 2040
QY 608 -----GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGly 624
Db 2041 AAGAGCCGAGCGCGCGCCCGCTACACAGCCGGAAGACGCGGAG----- 2091

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QY 625 SerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsn1leSerArgGlyLeu 644
Db 2092 CATGTGACAGGACGAGCGCTGATGTCAAGATGTGCGGCTCCAGAGCTCCAGGGC--- 2148
QY 645 GlnPhe1leLeuThrProAsnGlnPheSerAlaGlnThrPheTyrAlaLeuSerProThr 664
Db 2148 ----- 2148
QY 665 MetHisSerGlnAlaThrGlnValPro1leSerGlnSerAspLysSerAlaValAlaAla 684
Db 2148 ----- 2148
QY 685 ThrAsnThr1leAlaAsnGln1leAsnThrAlaProLysProAlaAlaProThrThrLeu 704
Db 2149 -----CAGAACTTCTCGGCGCCCGCGCGCGCC---CTGTCT 2187
QY 705 Gln1leProPro-----ProLeuProAla1leLysHis 715
Db 2188 CAGTGTCCGCTCCACCTCTCTGACAGCACAGAGCCAGCCGCG-CCAGGGCCACGGGCAC 2246
QY 716 LeuProArg-----ProGluThr-----LeuHis-ProAsnProAlaGlyLeuGlnG1 731
Db 2247 CTCCTCCGTGGGGACACAGGCTCTCTGTGCGCATCCCGCGCGCTGCCACAGAGCG 2306
QY 731 user1leSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaG1 751
Db 2307 GTCCCTGTCCGCTTACGCGCGGCGCAACCGCGCAGCATGAGTTCGTGGCGCAGAGGA 2366
QY 751 nSerAsnLeuThrLys-----AspArgSerMetArgLysSerPheAspMetGlyGlyG1 769
Db 2367 CACCCCGGCTGACGAGGCCCGCCGAGGGAGACCTCGGGAGACAC-----GA 2411
QY 769 uThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValG1 789
Db 2412 CACGTCCATCTCCATCCGCTCGGTGACAGAGAGAGAGTGTGCTTCTGAGGGCTT 2471
QY 789 nAsnLeu1leArgSerThrGluGlnLeuAsn 799
Db 2472 CAGCATCTCCAGTCCAGTCCAAAGAGAACCTTGAT 2502

RESULT 3
US-09-105-058C-22
; Sequence 22, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blannar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT FILING DATE: 1998-06-26
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
; US-09-105-058C-22

Alignment Scores:
Pred. No.: 3,32e-166 Length: 2169
Score: 1790.50 Matches: 390
Percent Similarity: 65.16% Conservative: 72
Best Local Similarity: 55.01% Mismatches: 146
Query Match: 39.38% Indels: 101
DB: 4 Gaps: 18

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[illegible]

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 7,43e-164 | Length: | 2273 |
| Score: | 167.00 | Matches: | 394 |
| Percent Similarity: | 63.40% | Conservative: | 79 |
| Best Local Similarity: | 52.82% | Mismatches: | 184 |
| Query Match: | 38.86% | Indels: | 90 |
| DB: | 4 | Gaps: | 17 |

US-09-810-796-5 (1-888) x US-09-177-650-88 (1-2273)

| | | | |
|----|-----|---|------|
| OY | 17 | AlAlaAlaArglyAspArglyLeuLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGly | 36 |
| Db | 100 | TCACACGCGCAGCGCCNCNCTATCGCGGGGCTCCAGACGCCCAAG-----CGC | 150 |
| OY | 37 | GlyGlyGlyLeuArgGlySerArgArgGlyLySGlnGlyAlaArgMetSerLeuGly | 56 |
| Db | 151 | GGCANCNNTNTTGACCAAGCGCCGACGGCGCGCGCGGANC-----GGG | 195 |
| OY | 57 | LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValTyrTrpArgVal | 76 |
| Db | 196 | AAGCCCCCNMA-----CGCAACGCCCTTCAACCCAACTG | 231 |
| OY | 77 | GlnAsnTyrLeuTyrAsnValLeuGlnArgProArgLysThrAlaPheIleTyrHisAla | 96 |
| Db | 232 | CAGAAATTCCTCTCAACGTCCTAGACCGGCCCGCGGCTGGGCTCACTACCAAGCC | 291 |
| OY | 97 | PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu | 116 |
| Db | 292 | TACGTGTTCCTCGGTTTTCCTCGCTGTGTCTTCTGTGTCTTCCACCACTCAAGAG | 351 |
| OY | 117 | HisThrIysLeuAlaSerSerCysLeuLeuLeuGlnPheValMetIleValPhe | 136 |
| Db | 352 | TACAGAAAGACCTCTGAGGGGCCCTTACATCTGGAAATCGGATACGTGATATC | 411 |
| OY | 137 | GlyLeuGlnPheIleIleArgGlyIleTrpSerAlaGlyCysCysArgTyrArgGlyTyr | 156 |
| Db | 412 | GGTTTAGTACTTGTGAGGATGTGGGCTGCAGGGCTGTGGCGGATGCAAGGTGG | 471 |
| OY | 157 | GlnGlyArgLeuArgPheAlaArgGlyProPheCysValIleAspThrIleValLeuIle | 176 |
| Db | 472 | AGGGGACGAGCTCAAGTTTGGCAGGAACCGTTCTGTGTGATGATACAGTGCATTT | 531 |
| OY | 177 | AlaSerIleAlaValIleSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu | 196 |
| Db | 532 | GCCCACTTCCTGGCGGGCTGGTGTCCAGGCGCAATCTTTGGCAATCTGCCGCTT | 591 |
| OY | 197 | ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetSparArgGlyGlyTyr | 216 |
| Db | 592 | CGGAGCTTGGCGTTCTTGCAAAATCTTCCGATGATCCGTATGGACCGGAGGGTGCACC | 651 |
| OY | 217 | TrpLysLeuLeuGlySerValIleTyrAlaHisSerLysGlnLeuIleThrAlaTrpTyr | 236 |
| Db | 652 | TGGAAAGCTTGGGATCGTATGTTACGCTCACAGCAGAGAGCGTGGTGCTGTGATC | 711 |
| OY | 237 | IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla | 256 |
| Db | 712 | ATTGGCTTCCTGCCCTCCACCTGCGCTCATTTCTGTGACTTGGCAGAAAGGCTGAG | 771 |
| OY | 257 | AsnLysIlePheSerTyrTyrAlaAspAlaLeuTrpIleTrpIleThrIleLeuThrTr | 276 |
| Db | 772 | AATGACCACTTGTACACCTACGAGATGACCTGTGGGGGCTGTGATCAACCTCGAGACC | 831 |
| OY | 277 | IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe | 296 |
| Db | 832 | ATTGGCTAGGGGACAGTACCTCCAGACCTGGAACGGAGGCTGCTGCAGCGACTTT | 891 |
| OY | 297 | AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla | 316 |
| Db | 892 | ACCCCTCATTTGGTCTCGCTTCTTGGCTCTCCGGCTGGCATTTTGGATCCGGCTTGGC | 951 |
| OY | 317 | LeuLysValGlnGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAla | 336 |
| Db | 952 | CTGAAGATCCAAAGACGACATCGGCAAAACATTTGAGAAACGGCGGAACCTCGCGCA | 1011 |

| | | | | |
|----|------|--|-------|--------------|
| QY | 337 | AsnLeuIleIecIncysValITPrpArgSerTyrAlaAlaasp | ----- | 349 |
| | | | | ::: |
| Db | 1012 | GGTGTATTCAGTCGTGCCCTGGAGATTGTATGCTACCTTCACGCCACCGACCTGCAC | ----- | 1071 |
| QY | 350 | ----- | ----- | ----- |
| | | ----- | ----- | ----- |
| Db | 1072 | TTCACGTGGCAGTACTACAGACGGACAGTCACTTCCCATGTACAGCTCAAAACTCA | ----- | 1131 |
| QY | 364 | ----- | ----- | ----- |
| | | ----- | ----- | ----- |
| Db | 1132 | ACCTATGGGCGCTTCACACATCATCCCACTCTGCACACCGCTGCAGATCTC | ----- | 1191 |
| QY | 374 | ----- | ----- | ----- |
| | | ----- | ----- | ----- |
| Db | 1192 | AAACAGCAAACTCTGGACTCACCCTTCAGGAAGAGCCACACGACCATCACCAGCCCC | ----- | 1251 |
| QY | 387 | ArgGlyIeSerIleIysSerArgAlaIaSerValIasp | ----- | ArgArgSerPro |
| | | | | |
| Db | 1252 | CGAGGATGGCTCCCAAGGAAGGGGCTTCCACGCGCCAGACGGTCCGGCGGCCCC | ----- | 1311 |
| QY | 405 | SerThrAspIleThrAlaGluGlySerProThrIysValGlnIysSerTyrSerPheasn | ----- | 424 |
| | | | | |
| Db | 1312 | AGGCGGATCAGAGTCTGTATGACAGCCGACAGCAAGGTGCCAAGCTGGAGCTTGCT | ----- | 1371 |
| QY | 425 | AspArgThrArgPheArgProSerLeuArgLeuIysSerSerGlnProIysProValIle | ----- | 444 |
| | | | | |
| Db | 1372 | GACCGCAGCGGCACACGCCAGGCTTCCGATCATCAAGGCTCTGCATCCCGCACAATTCA | ----- | 1431 |
| QY | 445 | AspAlaIaSPThrAlaLeuGlyThrAspAspValTyrAspGlnIysGlyCysGlnCysasp | ----- | 464 |
| | | | | |
| Db | 1432 | GAAGAAGCAAGCTCCCTGGGGAGGATGTCAGAGACAAACAGACTGTACATGGCAG | ----- | 1491 |
| QY | 465 | ValSerValGluIaSPleuThrProProLeuIysThrValIleArgAlaIleArgIleMet | ----- | 484 |
| | | | | |
| Db | 1492 | TTTGTGACAGAACTTACCTTACCCTGGCGCTCAAGTATGACATCAGAGCGTGTGTATG | ----- | 1551 |
| QY | 485 | LysPheHisValAlaIaIysArgIysPheIysGluThrLeuArgProTyrAspValIysasp | ----- | 504 |
| | | | | |
| Db | 1552 | CGGTTCTTGATCTAAAGCAAAAGTTCAAAGAGAGTCTGCCCATGTGATGATGAGAC | ----- | 1611 |
| QY | 505 | ValIleGluGlnTyrSerAlaIaIysIleAspMetLeuIysArgIleIysSerLeuGln | ----- | 524 |
| | | | | |
| Db | 1612 | GTCATCGACAGTACCTCGCTGACACTTGCATATGTGTCCCGCATCAGAGCCTGCAG | ----- | 1671 |
| QY | 525 | ThrArgValaSPGlnIleLeuGlyIysGlyGlnIleThrSerAspIysLysSerArgGlu | ----- | 544 |
| | | | | |
| Db | 1672 | ACCAGAGTGGACAGATTTGTGGCGGGGCCCAACATATACGAT-- | ----- | 1728 |
| QY | 545 | LysIleThrAlaGluIaSPGlnThrThrAspIleuSerMetLeuGlyArgValValLys | ----- | 564 |
| | | | | |
| Db | 1729 | AAAGGCCACGGGAAACGGAGCTGCCCGGAAGACCCACGATGAGGAGCGGCTTGGGAAG | ----- | 1788 |
| QY | 565 | ValGluIysGlnValGlnSerIleGlnIleuSerLysIleuAspCysLeuAspIleTyrGln | ----- | 584 |
| | | | | |
| Db | 1789 | GTGGAACAAACAGGTCTTGTTCATGAAAGAGAGCTGACTTTGTGGAGACATCTATACA | ----- | 1848 |
| QY | 585 | GlnValaIleuArgIysGlySerAlaIaSerAlaLeuAlaIeuaIaSerPheGlnIleProPro | ----- | 604 |
| | | | | |
| Db | 1849 | CAG----- | ----- | ----- |
| | | ----- | ----- | ----- |
| QY | 605 | PheGluCysGlnGlnThrSerAspTyrGlnSerProValaSPerLysaspIleuSerGly | ----- | 624 |
| | | | | |
| Db | 1900 | ---GAGCCTGAGCGCGCACACCCTTACACAGCCCGAGAGACAGCGCTGAC----- | ----- | 1947 |
| QY | 625 | SerAlaGlnAsnSerGlyCys----- | ----- | ----- |
| | | ----- | ----- | ----- |
| Db | 1948 | CATGACAGAACACATGGCTGTATCATTAAGATGTCTCGCTCACACAGCTCTACGG--GCC | ----- | 2005 |
| QY | 642 | ArgGly----- | ----- | ----- |
| | | ----- | ----- | ----- |
| Db | 2006 | AAAGGACTACGCACGACCCCAAGCATCCCGCTCCAGTGTCTCTCCCTCCACACTCGT | ----- | 2065 |
| QY | 653 | PheSerAlaGlnThr----- | ----- | ----- |
| | | ----- | ----- | ----- |


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QY 457 AspGluysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuysThr 476
    ::::::::::::::::::::
Db 1438 GAAGCAGAGGGGTATGGGAATGACTTCCCATCGAGACATGATCCCATCCAGCCGGAAGGCC 1497
QY 477 ValLeaGalaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThr 496
    ::::::::::::::::::::
Db 1498 GCCATCCGAGCGGTGAGATCTACAAATCCGTCCTATATAAAAAAATTTCAAGGAGACT 1557
QY 497 LeuArgProLysAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMet 516
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Db 1558 TTGAGGCCCTTACGATGATGAGATGTGATTGAGCATTTCTCCCGCATCTCGACATG 1617
QY 517 LeuGlyArgIleLysSerLeuThrArgValAspGlnIleLeuLysGlyGlnIle 536
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Db 1618 CTTTCAGAGATTAAGTACTTTCAGACGAGATATGATATTTCACCCCTGACCTCC 1677
QY 537 ThrSerAspLysLysSerArg----- 543
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Db 1678 TCCAGCGCCAAACACAGAGCTCAGAAAGGTCAGATTCACCTTCCCATCCAGCAA 1737
QY 544 -----GluLysIleThrAlaGlnHisGluThr-----AspAspLeuSer 557
    ::::::::::::::::::::
Db 1738 TCTCCCAAGAAATGAAACCATATGATAGCCAGACCATCATCAGAAATCGAAACCAAGC 1797
QY 558 MetLeuGlyArgValAlaLysValGluLysGlnValGlnSerIleGluSerLysLeuAsp 577
    ::::::::::::::::::::
Db 1798 ATGATGGGGAGATTGTGTAAGTTGTAAGACAGGTTCAGACATGGGGAAGACGCGGAC 1857
QY 578 CysLeuLeuAspIleTyrGlnGlnValLeuArg----- 588
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Db 1858 TTCTCTGTGATGATGACATCGACACATGGAACGGTTCAGCTCAGGTCCAGTCAAGTAT 1917
QY 589 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPhe 605
    ::::::::::::::::::::
Db 1918 TACCCACCAAGGCGACTCTCTCG-----CCAGCT 1947
QY 606 GluCysGlnGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerLys 625
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Db 1948 GAAGCAGAGAGAGAGAGAGACATGATTCG--GATTGAAAACATCATCTGCAAC 2004
QY 626 AlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGln 645
    ::::::::::::::::::::
Db 2005 TATTCTGAGACAGGCCCCCGGAACACCATCAGCTTCAC----- 2046
QY 646 PheIleLeuThrProAsnGlnPheSerAlaGlnThrPheTyrAlaLeuSerProThrMet 665
    ::::::::::::::::::::
Db 2047 ---CAGGTGACCATTTGACAAAGTACAGCCCTATGGGTTTTCACATGACCT----- 2097
QY 666 HisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAlaThr 685
    ::::::::::::::::::::
Db 2098 -----GTGAACCTGCCCCCGAGGGGAGCCAGTTCTGGAAGGTTGACAGCACT 2145
QY 686 AsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrLeuGln 705
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Db 2146 -----CCTCTCTCTCTAGCAACACCTATGTTGAG 2175
QY 706 IleProProLeuProAlaIleLysHisLeuProArgProGlnThrLeuHisProAsn 725
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Db 2176 AGGCCCAAGGTCCTGCTATCTGACCTTCTGACACCCAGAGAGAGTGGCAC---TCC 2232
QY 726 ProAlaGlyLeuGlnGlnSerIleSerAspValThrThrCysLeuValAlaSerLysGlu 745
    ::::::::::::::::::::
Db 2233 CAGGCTGACCTGAGGAGCCCTACTCTGAC----- 2262
QY 746 AsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAsp 765
    ::::::::::::::::::::
Db 2263 CCAATTTCCCGCGGAG-----AGACGTACGATCAGC 2295
QY 766 MetGlyGlyGlnThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSer 785
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Db 2296 CGAGACAGTGAACACACTGTGTCCTG----- 2322

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QY 786 LeuSerValGlnAsnLeuIleArgSerThrGluLeuAsnIleGlnLeuSerGlySer 805
    ::::::::::::::::::::
Db 2323 ATGTGCGCAACAC-----GAGAGCTGAGAGGTCATCCAGTGGCTTC 2367
QY 806 GluSerLysSerArgGlySerGlnAspPheTyrPro-----LysThrArg 821
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Db 2368 AGCATCTCCAGACAGACAGATATATGTGTGCGCCCAATGGCGGTGAGCTGATG 2427
QY 822 GluSerLysLeuPheIleThrAspGluValGlyProGluGlnThrGluThrAspThr 841
    ::::::::::::::::::::
Db 2428 AGGAGAGAGCGCTACCTCGCGGAG-----GCTGAGAGGACACAGACAGGACCC 2478
QY 842 Phe 842
    ::::::::::::::::::::
Db 2479 TTC 2481

RESULT 7
US-09-177-650-6
; Sequence 6; Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

Alignment Scores:
Pred. No.: 5.5e-146 Length: 2914
Score: 1587.50 Matches: 386
Percent Similarity: 54.61% Conservative: 106

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Best Local Similarity: 42.84% Mismatches: 244
Query Match: 4 Indels: 165
DB: 4 Gaps: 28
US-09-810-796-5 (1-888) x US-09-177-650-6 (1-2914)
QY 3 AspValGlnSerGlyArgGlyValLeuLeuAsnSerAlaAlaArgGlyAspGly 22
DB 163 GAGCTGGAGCA-----GTCACCTTGCGCTGGGGCGGACCGACAAAGACGG 213
QY 23 LeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlu 42
DB 214 ACCCTGCTGCTG-----GAGGGCGGGCGCGGACGAGGGG 249
QY 43 SerArgArgGlyGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
DB 250 CACGGGAGACCCCGCAGCGC-----ATCGGCTCCCGCCCAACACCCCGCTGAGCGCC 303
QY 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
DB 304 CCAAGTCAG-----AGAACACAGCCCAAGTACCGCGCATCAAACTTGATCTAC 354
QY 82 AsnValLeuGluArgProArgGlyTyrPalAphHeileTyrHisAlaPheValPheLeuLeu 101
DB 355 GAGCCCTGGAGACACCGGGCGCTGGCGCTTACACAGCGTGGTGTCTGATT 414
QY 102 ValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGlnHisThrLysLeuAla 121
DB 415 GTCTGGGGTCTTGATTCGTGGCTGCTCCGACACATTCAGCAAGATATGAGACTGCTCG 474
QY 122 SerSerCysLeuLeuIleLeuGlnPheValMetIleValIleValPheGlyLeuGlnPheIle 141
DB 475 GGAAGCTGGCTTCTGTTACTGAGACATTTGCTATTTTCATCTTTGGAGCCAGTTTGT 534
QY 142 IleArgIleTyrSerAlaGlyCysCysArgTyrArgIlyTyrGlnGlyArgLeuArg 161
DB 535 TTGAGATCTGGCGCTCGCGATGTGTGCGGATCAAAAGCGTGGCGGCGACGAGAG 594
QY 162 PheIleArgLysProPheCysValIleAspThrIleValIleAlaSerIleAlaVal 181
DB 595 TTTCACAGGAAGCCCGTGCATGTGGCATCTTTGCTGATTTGCTCTGTGCGAGTGC 654
QY 182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
DB 655 GTTGCTGTGGAAACCAAGCAATGTTCTGGCACCTCC---CTGGAAAGCCTGGCGCTTC 711
QY 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyLysThrTyrLysLeuLeuGly 221
DB 712 CTGCAAGATCCGCGCATGCTCGGATGGACCGGAGGTGCACCTGGAAGCTTCTGGGC 771
QY 222 SerValValTyrAlaHisSerLysGlnLeuIleThrAlaTyrTyrIleGlyPheLeuVal 241
DB 772 TCACCACTCTGTGCCACAGCAAGAACTCATCAGCGCTGGTACATCGTTCTCTGACA 831
QY 242 LeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla----- 256
DB 832 CTCATCTCTTCTTCATTTCTGTCTACTGTTGAGAAAGAGTCCACAGAGTGATGCA 891
QY 257 -----AsnLysGlnPheSerThrTyrAlaAspAlaLeuTyrTrpGlyThr 271
DB 892 CMAAGAGAGAGATGAAGAGAGAGTTTGAGACCTATGCGATGCGCTTGCGGGCGCTGC 951
QY 272 IleThrLeuThrTrpIleGlyTyrGlyAspLysThrProLeuThrTyrLeuGlnArgLeu 291
DB 952 ATCAACATGGCCACCATTTGGCTATGGAGACACAGACCCAAACGCGGAGAGCGCTCTG 1011
QY 292 LeuSerAlaGlyPheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyLysLeu 311
DB 1012 ATGGCCGCGACCTTTCTTAATTTGCGCTCTCTTTTGGCCCTTCACAGCGGCGCATCTGC 1071
QY 312 GlySerGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGlyLysArg 331
DB 1072 GGGTCCGGGCTGGCCCTCAAGGTGAGAGCAACCGTCAAGAGCACTTTGAGAAAGG 1131

QY 332 ArgAsnProAlaAlaAsnLeuIleGlnCysValTyrPargSerTyrAlaAlaAspGluLys 351
DB 1132 AGAAGCCAGACTGCTGAGCTCATTTACAGCTGCTGGAGGTATTTGCTACCAACCCCAAC 1191
QY 352 SerValSer---IleAlaThrTrpLys-----ProHisLeu 362
DB 1192 AGGATTTAGCTGCTGGGACATGGAGATTTTATGATCAGTCGTCCTTTCTCTTCTTC 1251
QY 363 LysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArgValArg 382
DB 1252 AGGAAGAAACAGCTGGAGGAGCATCCAGCCAAAGCGTGGCTCTTGGAGGCGGTGCG 1311
QY 383 MetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArg 402
DB 1312 CTCTTCAATCTGCTGTGATCAATCTAA-----GGAACGATATT 1353
QY 403 SerProSerThrAspIleThrAlaGlnGlySerProThrLysValGlnLysSerTrpSer 422
DB 1354 ACCCTCTGAATGATGATGCGCATGAGAAAGATCTCTTAAAGAACCAACCAAGCTGTGCG 1413
QY 423 PheAsnAspArgThrArgPheArgProSerLeuArgLeuLys----- 436
DB 1414 TTAAACATATAAGAGCTTTCCGCGCGCTTCGCAATGAAAGCCTACGCTTGTGCGAG 1473
QY 437 SerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyr 456
DB 1474 AGTTCGAA-----GATGCCGCGACAGT-----GACCCCATGGCG 1509
QY 457 AspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThr 476
DB 1510 GAAGACAGGGCGTATGGAAATGACTTCCCATCGAAGACATGATCCACCTGAGGCC 1569
QY 477 ValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGlnThr 496
DB 1570 GCCATCGACCGCGCAATTCATCAATTCGCTCTATAAAAAAATTCAGAGAGACT 1629
QY 497 LeuArgProTyrAspValLysAspValIleGlnLysThrSerAlaGlyHisLeuAspMet 516
DB 1630 TTGAGGCTTAACATGTAAGAGATGTGATGAGCAGTATTCGCGGCGCATCTGCACATG 1689
QY 517 LeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIle 536
DB 1690 CTTTCAGGATTAAGTACCTTCACAGCAAGATATGATTTTCACCCCTGAGACTCCG 1749
QY 537 ThrSerAspLysLysSerArg----- 543
DB 1750 TCCAGCGCCAAACCAAGAACTTCAGAAAGGTCACGATTCACCTCCATCCACGCA 1809
QY 544 -----GluLysIleThrAlaGlnHisGlnThr-----AspAspLeuSer 557
DB 1810 TCTCCCAAGATGAACCATATGTAGCCAGACCATCCACATCAGAAATGGAAGACCAAGC 1869
QY 558 MetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGlnSerLysLeuAsp 577
DB 1870 ATGATGGGGAAGTTGTAAAGAGTTGAAAGACAGGTTCAGCATGGGAGAGAGCTGGAC 1929
QY 578 CysLeuLeuAspIleTyrGlnGlnValLeuArg----- 588
DB 1930 TTCCTCGGATATGACATGCAACATGAGACGTTGCAAGTCCAGTCCAGTCCAGAGAT 1989
QY 589 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPhe 605
DB 1990 TACCAACCAAGGACACTCTCTCG-----CCAGCT 2019
QY 606 GluLysGlnGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySer 625
DB 2020 GAAACAGAGAGAGAGAGCAACAGCATTTCC---GATTTGAAACCATCATCTGCAAC 2076
QY 626 AlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGln 645
DB 2077 TATTCTGAGACAGGCCCCCGGAACCACTTACAGCTTCCAC----- 2118

Alignment Scores:

Pred. No.: 1,93e-109 Length: 900
 Score: 1207.50 Matches: 227
 Percent Similarity: 83.88% Conservative: 28
 Best Local Similarity: 74.67% Mismatches: 40
 Query Match: 26.56% Indels: 9
 DB: 4 Gaps: 2

US-09-810-796-5 (1-888) x US-09-105-058C-5 (1-900)

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QY 56 GLYLSProLeuSerYrTrhSerSerGlnSerCysArgAArgAsnValLysYrArgArg 75
DB 13 GGGAAAGCCC-----CCGAAGCCCAAGCCCTTCTACCGCAAG 48
QY 76 ValGlnAsnTYrLeuTYrAsnValLeuGlnArgProArgGlyTPAlaPheIleYrHis 95
DB 49 CTGCAGAAATTCTCTACAGAGCTGCTAGAGCGGCCCGCGCTGGCGTTCATCTACAC 108
QY 96 AlAphValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIlePro 115
DB 109 GCCTACGCTGCTCTTATGCTTCTCTCCGCTTGTGCTTGTTCACACATCAAG 168
QY 116 GlnHisThrLeuAlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValVal 135
DB 169 GAGTACGACAGAAAGACTCTGAGGGGCCCTTACATCTTGAAATGCTGACTATGCTGTA 228
QY 136 PheGlyLeuGlnPheIleIleArgIleTPSerAlaGlyCysCysArgTYrArgGly 155
DB 229 TTGCGTGTGAGTCTTGTGAGATCTGGCGTGCAGCGCTGCTGTCGCGATGAGAGC 288
QY 156 TrpGlnIlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeu 175
DB 289 TGGAGGGGCGAGGCTCAAGTTGGCCAGGAAGCGTCTGTGATGATATCATGAGTGGCTG 348
QY 176 IleAlaSerIleAlaValAlaSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAla 195
DB 349 ATTCGCCATTCGCTGCTGCTGCTGCTGCTGCCAGGCAATGCTTTGCCACATCTGCG 408
QY 196 LeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGly 215
DB 409 CTTCGGAGCTTGCCTGCTCTTCCAAATCTTGGGAGATGCCATGACCGGAGCGCTGCG 468
QY 216 ThrTrpLysLeuLeuGlySerValValTYrAlaHisSerLysGlnLeuIleThrAlaTrp 235
DB 469 ACCGGAAGCTCTTGGGATCGGTAAGTCTACGCTCACAGCAAGAGAGTGTGACTGCTGG 528
QY 236 TYrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTYrLeuValGlnLysAsp 255
DB 529 TACATGGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
QY 256 AlaAsnLysGlnPheSerThrTYrAlaAspAlaLeuTPTrpGlyThrIleThrIleThr 275
DB 589 GAGATGACCACTTGGACCTACACAGATGACCTGGTGGGCTGCTGCTGCTGCTGCTG 648
QY 276 ThrIleGlyTYrGlyAspLysThrProLeuThrTPLeuGlyArgLeuLeuSerAlaGly 295
DB 649 ACCATTTGGCTACGGGACAAAGTACCTCAGACCTGGAAGGAGAGGTGCTGGCAGGAC 708
QY 296 PheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPhe 315
DB 709 TTTACCTCATTTGGTGTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
QY 316 AlaLeuLysValGlnGlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAla 335
DB 769 GCCCTGAAAGTCCAGACAGCATGCGCAAAACATTTGAAAGAGGGGGAACCTCTGG 828
QY 336 AlaAsnLeuIleGlnCysValTYrPArgSerTYrAlaAlaAspGlnLysSerValSerIle 355
DB 829 GCAGTCTGATCTCAGTCTGCTGCTGAGATTTCTATGCTACTAACCTTCACGACCGAC 888
QY 356 ---AlaThrTrp 358
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DB 889 CACTCCAGCTGG 900
RESULT 10
US-09-105-058C-3
; Sequence 3, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blamar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grubkoif, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105, 058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-09-105-058C-3
Alignment Scores:
Pred. No.: 7.52e-109 Length: 900
Score: 1201.50 Matches: 226
Percent Similarity: 83.55% Conservative: 28
Best Local Similarity: 74.34% Mismatches: 41
Query Match: 26.42% Indels: 9
DB: 4 Gaps: 2
US-09-810-796-5 (1-888) x US-09-105-058C-3 (1-900)
QY 56 GLYLSProLeuSerYrTrhSerSerGlnSerCysArgAArgAsnValLysYrArgArg 75
DB 13 GGGAAAGCCC-----CCGAAGCCCAAGCCCTTCTACCGCAAG 48
QY 76 ValGlnAsnTYrLeuTYrAsnValLeuGlnArgProArgGlyTPAlaPheIleYrHis 95
DB 49 CTGCAGAAATTCTCTACAGAGCTGCTAGAGCGGCCCGCGCTGGCGTTCATCTACAC 108
QY 96 AlAphValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIlePro 115
DB 109 GCCTACGCTGCTCTTATGCTTCTCTCCGCTTGTGCTTGTTCACACATCAAG 168
QY 116 GlnHisThrLysLeuAlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValVal 135
DB 169 GAGTATGAGAAAGACTCTGAGGGGCCCTTACATCTGGAATGTAATGCTGCTG 228
QY 136 PheGlyLeuGlnPheIleIleArgIleTPSerAlaGlyCysCysArgTYrArgGly 155
DB 229 TTTCGCTGAGTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
QY 156 TrpGlnIlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeu 175
DB 289 TGGAGGGGCGGCGCTCAAGTTTCCCGGAAACCTCTGATGATGACATCATGCTGCT 348
QY 176 IleAlaSerIleAlaValAlaSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAla 195
DB 349 ATCCCTTCATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408
QY 196 LeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGly 215
DB 409 CTCCGGAAGCTTGCCTTCTCAGATTTCTGCGGATGATGCCATGACCGGAGGAGG 468
QY 216 ThrTrpLysLeuLeuGlySerValValTYrAlaHisSerLysGlnLeuIleThrAlaTrp 235

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Db 469 ACCTGGAAGCTGCGGCTGTGTGTCATGCCACAGACAGACCTGTGCTGCTG 528
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Qy 236 TTTTLLGGTlPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAsp 255
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Db 529 TACATCGGCTCTTCTTCTGTCATCTGACCTGCTGCTGCTGCTGCTGCTGCTG 588
|||
Qy 256 AlaAsnLysGluPheSerTrpTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThr 275
|||||
Db 589 GAGAAGACACCTTGTGACACTACCGGATGCTGCTGCTGCTGCTGCTGCTGCTG 648
|||
Qy 276 ThrIleGlyTyrGlyAspLysTyrProLeuThrTrpLeuGlyArgLeuLeuSerIle 295
|||||
Db 649 ACCATTGGCTACGCGGAGCAATGACCCACAGACCTGGAACGCGACGCTCTGGCCAA 708
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Qy 296 PheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPhe 315
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Db 709 TTTACCTCTACCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 768
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Qy 316 AlaLeuLysValGlnGlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAla 335
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Db 769 GCCCTGAAGGTTGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 828
|||
Qy 336 AlaAsnLeuIleGlnGlyValTyrPargSerTyrAlaAlaAspGluLysSerValSerIle 355
|||||
Db 829 GCAGGCTGTATCCAGTCGGCTGAGATTTCACCCACCAACCTCTGCGCAGACAGCTG 888
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Qy 356 ---AlaThrTrp 358
|||
Db 889 CACTCCACGCTG 900
|||

RESULT 11
US-09-135-021-1
; Sequence 1, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: A HOMODYOUS MUTATION IN KVLQTL WHICH CAUSES JERVELL
; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
; FILE REFERENCE: 2323-128
; CURRENT APPLICATION NUMBER: US/09/135, 021A
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/874, 655
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/094, 477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (163)..(2190)
US-09-135-021-1

Alignment Scores:
Pred. No.: 1,6e-99 Length: 3181
Score: 1116,50 Matches: 294
Percent Similarity: 52,75% Conservative: 118
Best Local Similarity: 37,64% Mismatches: 247
Query Match: 24,55% Indels: 122
Gaps: 23

US-09-810-796-5 (1-888) x US-09-135-021-1 (1-3181)
Qy 7 GlyArgGlyArgValLeu---LeuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeu 25
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Db 189 GCGCCAGAGGAAAGCGCTGGGGTGGGCGGCTGCGAGCGCGCGCGCGCGCGCGG 248
|||
Qy 26 LeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyGlyLeuArgLysArgArg 45
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Db 249 CTTGGCCAGAGACTGCCCTTCTCTGCTGAGCTGGCGAGGGCGCGCGCGCGCGCG 308
|||
Qy 46 GlyLysGlnGlyAlaArgMet----- 52
|||
Db 309 GCTCTACAGCCCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 368
|||
Qy 53 -----SerLeuLeuGlyLysProLeu-Se 60
|||
Db 369 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 428
|||
Qy 60 rTyrTrpSerSerGlnSerCysArgArgAsnValLysTyrArg---ArgValGlnAsn 79
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Db 429 GCGCGCTCTCATCTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 488
|||
Qy 79 rLeuTyrAsnValLeuGlnArgProArgGlyTrp---AlaPheIleTyrHisAlaPhe 98
|||
Db 489 CGTCTACACTTCTCTGAGCGTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 548
|||
Qy 98 lPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHis 118
|||
Db 549 CTTCCTCATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 608
|||
Qy 118 rLysLeuAlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValValPheGly 138
|||
Db 609 CGCCCTGGCGACGCGGAGCTCTTCTGATGAGATCTGCTGCTGCTGCTGCTGCTG 668
|||
Qy 138 uGluPheIleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGln 158
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; CURRENT FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: 60/094,477
 ; PRIOR FILING DATE: 1998-07-29
 ; PRIOR APPLICATION NUMBER: 08/921,068
 ; PRIOR FILING DATE: 1997-08-29
 ; PRIOR APPLICATION NUMBER: 08/739,383
 ; PRIOR FILING DATE: 1996-10-29
 ; PRIOR APPLICATION NUMBER: 60/019,014
 ; PRIOR FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 3181
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (163)..(2190)
 ; US-09-135-010A-1

Alignment Scores:
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 Score: 1116.50 Matches: 294
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US-09-810-796-5 (1-888) x US-09-135-010A-1 (1-3181)

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; Patent No. 6420124
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Conners, Timothy D.
; APPLICANT: Burd, Timothy C.
; APPLICANT: Spiawski, Igor
; TITLE OF INVENTION: KVIDT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,735
; EARLIER FILING DATE: 2000-06-19
; EARLIER APPLICATION NUMBER: 09/135,010
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (163)..(2190)
US-09-597-735-1

Alignment Scores:
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Score: 1116,50 Matches: 294
Percent Similarity: 52,75% Conservative: 118
Best Local Similarity: 37,64% Mismatches: 247
Query Match: 24,55% Indels: 122
Gaps: 23

US-09-810-796-5 (1-888) x US-09-597-735-1 (1-3181)
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Db 189 GGCAGAGAGAGAGAGCGGTGGGTGGGCGCCGCTGCGCAGGCGCGCGCGGAGACGCGG 248

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GenCore version 5.1.3
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Run on: January 11, 2003, 18:00:47 ; Search time 82 Seconds
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Title: US-09-810-796-5

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 4547 | 100.0 | 3111 | 10 | US-09-825-147-3 |
| 4 | 4527.5 | 99.6 | 2694 | 10 | US-09-810-796-2 |

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| 6 | 4513.5 | 99.3 | 3074 | 10 | US-09-813-148-1 | Sequence 1, Appli |
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| 8 | 1790.5 | 39.4 | 2169 | 9 | US-10-128-870-22 | Sequence 22, Appl |
| 9 | 1587.5 | 34.9 | 2565 | 9 | US-10-128-870-26 | Sequence 26, Appl |
| 10 | 1507.5 | 26.6 | 900 | 9 | US-10-128-870-5 | Sequence 5, Appli |
| 11 | 1201.5 | 26.4 | 900 | 9 | US-10-128-870-3 | Sequence 3, Appli |
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| 18 | 290 | 6.4 | 429 | 10 | US-09-783-590-4509 | Sequence 4509, Ap |
| 19 | 262 | 5.8 | 1979 | 10 | US-09-864-761-3784 | Sequence 3784, Ap |
| 20 | 260.5 | 5.7 | 1917 | 9 | US-10-024-623-12 | Sequence 12, Appl |
| 21 | 260.5 | 5.7 | 2847 | 9 | US-10-024-623-10 | Sequence 10, Appl |
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| 28 | 224 | 4.9 | 1792 | 10 | US-09-974-712-3 | Sequence 3, Appli |
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| 41 | 180.5 | 4.0 | 1740 | 9 | US-09-922-3644-15 | Sequence 15, Appl |
| 42 | 180.5 | 4.0 | 1740 | 9 | US-09-254-590-15 | Sequence 15, Appl |
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| 44 | 178 | 3.9 | 1740 | 9 | US-09-922-3644-21 | Sequence 21, Appl |
| 45 | 178 | 3.9 | 1740 | 9 | US-09-254-590-21 | Sequence 21, Appl |

ALIGNMENTS

RESULT 1
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; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; TITLE OF INVENTION: KCNO5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; NAME/KEY: CDS
; LOCATION: (1)...(2667)
; OTHER INFORMATION: KCNO5-2 coding sequence
US-09-810-796-3

Alignment Scores:

Pred. No.: 0
 Score: 4547.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 10

Length: 2667
 Matches: 888
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-810-796-5 (1-888) x US-09-810-796-3 (1-2667)

1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGly 20
 1 ATGAGAGATGTGGAGTGGCGGGGAGGAGGCTGCTGTAACCTCGGACCGGAGGAGG 60
 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
 61 GACGGCTGCTACTGCTGGGACCGCGCGGACGCTGGTGGCGGCGGCTGGCTG 120
 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
 121 AGGAGAGACCCCGGGGCAAGCAGGAGGCGCGGATGAGCTGCTGGGAGGAGCGCTCT 180
 61 TyrThrSerSerGlnSerCysArgArgArgValLysTyrArgArgValGlnAsnTyrLeu 80
 181 TACACGATACGACAGAGTGGCGGGCAACGTCAGTACCGGGGGGTCAGAACTACTG 240
 81 TyrAsnValLeuGluArgProArgGlyTyrPalaPheIleTyrHisAlaPheValPheLeu 100
 241 TACAACGCTGAGAGAGACCGCGGCTGGGCTGATCATCTACCCACTTCGTTTCTC 300
 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
 301 CTGTGCTTGTGCTGCTGATTTGTGACGTGTTTTCACCATCCCTGACGACAAATTTG 360
 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
 361 GCTCAAGTGGCTGCTGATCTGCTGAGTTCGATGATGATGCTGCTGTTGGTGGAGTTC 420
 141 IleIleArgGlyLeuSerAlaGlyCysCysArgTyrArgGlyTyrPalaGlyLeu 160
 421 ATCATTCGAATCTGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
 481 AGGTTGCTCGAAGACCCCTGCTGTTATAGATACCATGTTCTTATCGCTTCAATAGCA 540
 181 ValValSerAlaLysThrGlnLysAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
 541 GTTGTCTTCGAAAAAAGCTCAGGATATATTTTCCACGCTGCTCAGCAAGCTCTCCGT 600
 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyLysThrTyrPalaLeuLeu 220
 601 TTCTCAAGATCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
 661 GGTTCAGAGGCTTATAGCTCAGCAAGAAATTAATCAGACTGTAATAGATTTTGG 720
 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
 721 GTTCTTATTTTTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 261 SerTyrTyrAlaAspAlaLeuTyrPalaGlyThrIleThrLeuThrThrIleGlyTyrGly 280
 781 TCTACATATGCGAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 281 AspLysThrProLeuThrTyrPalaGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
 841 GACAAAGTCCCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
 901 ATTCTTCTTTCGACTCTCTGCGGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960

321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
 961 GAACAACACCGCCAGAAACCTTTGAGAAAAGAAAGAACCCAGCTCCACCTCATTTAG 1020
 341 CysValTyrPalaSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro 360
 1021 TGTGTTGGGTGATGATGCGACGCTGATGAGAAATCTGTTCCATTTGCAACTGGAAGCA 1080
 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
 1081 CACTTGAAGGCTTGGACACCTCGACGCTCAACATCAAGAGCTAGTTTAAAGAGCGCA 1140
 381 ValArgMetAlaSerProArgGlyLysSerIleLysSerArgGlnAlaSerValGlyLysP 400
 1141 GTGGCGATGGCTACCCAGGAGGCGCAGAGTAAAGACCGCAAGCTCAGTAGTGAC 1200
 401 ArgArgSerProSerThrAspIleThrAlaGluLysSerProThrLysValGlnLysSer 420
 1201 AGGAGTCCCCAACACCGACATCATACAGCCGAGGCGAGTCCACCAAGTGCAGAAAGAC 1260
 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
 1261 TGGAGCTTCAACGACGAAACCGCTTCCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1320
 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
 1321 AAACCACTGATGATGCTGATGACACAGCCCTTGCACTGATGATGATGATGATGATGATG 1380
 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
 1381 TGCCAGTGTGATGTATCAGTGAAGACCTCACCCACCACTTAAACGTCATTTGGAGCT 1440
 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
 1441 ATCAGAAATTAAGAAATTTCACTGTTGCAAAACGAAAGTTTAAAGAAACGTTAGCTCATAT 1500
 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
 1501 GATGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
 1561 AAAAGCCTTCAACACGCTGATCAATTTCTGGAAGGCGCAATTCATCAGTAGTAAG 1620
 541 LysSerArgGluLysIleThrAlaGluHisGlnThrAspPheLysSerMetLeuGly 560
 1621 AAGACCCGAGAAATTAACGACACACATGAGACACAGACATCTCAGTAGTGGCTGCT 1680
 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
 1681 CGGAGTGCAGAGTGAAGAAACAGGTACAGTCCATAGAGTCCAAAGCTGAGCTGCTACTA 1740
 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
 1741 GACATCTATCAACAGGCTCTTGGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
 601 GlnIleProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
 1801 CAGATCCACCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
 1861 GATCTTTCGGGTCCGCAAAACAGTGGCTCTTATCCAGATCAACATGCTGCTCCCAATC 1920
 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
 1921 TCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
 1981 CTACCCCTACTATGACAGTGAACACACAGGAGGCGCAATTAGTGAAGGCGATGGCTCA 2040
 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700

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Db 2041 GCATGGCAGCACCACACACATTGCACAAACAAATTAATACGGCACCCCAAGCCAGACGCC 2100
QY 701 ProthrlrleuglnlileproproleuProalalelyshlslleuproargploglu 720
Db 2101 CCACAACTTACAGATCCCACTCTCTCCACGCAATCAAGCATCTGCGCCAGGCCAGAA 2160
QY 721 ThrleuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrhrCysleu 740
Db 2161 ACTTCGACCCCTAACCCCTGCAGGCTTACAGGAAGCAATTTCTGACGTCAACCGCTGCTT 2220
QY 741 ValAlaSerIlyscIuaanValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2221 GTTGCCCTCCAAAGAAATGTTTCAGGTTCACAGTCACAAATCTCACCAAGACCGTTCTATG 2280
QY 761 ArgIlySerPheAspMetGlyGlyThrleuLeuSerValCysProMetValProLys 780
Db 2281 AGGAAAGCTTTGACATGACGAGAGAAACTCTGTTGTCTGTCTGCTCCATGCTGCGAGAG 2340
QY 781 AspleuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800
Db 2341 GACTTGGGCAAAATCTTGTCTGTGCAAAACCTGATCAGGTGACCGAGAACTGATATA 2400
QY 801 GluLeuSerGlySerGlySerSerGlySerArgGlySerGlnAspPheTyProLysTrp 820
Db 2401 CAATTTCAAGGAGTGAAGTCAAGTGGCTCCAGAGCCAGCAAGATTTTACCCCAAAATGC 2460
QY 821 ArgGlySerIlySerLeuPheIleThrAspGlyGluValGlyProGluGluThrGlnhrAsp 840
Db 2461 AGGGAATCCAAATTTGTTTATACATGATGAAGAAGTGGTCCCGAAGACACAGACAGAC 2520
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Db 2521 ACTTTGATGCCCCACGACGCGCTGCCAGGAAAGCTGCTTTCATCAGACTCTCTAAGG 2580
QY 861 ThrGlyArgSerArgSerArgSerGlnSerIleCysLysAlaGlyGlySerThrAspAlaLeu 880
Db 2581 ACTGGAAGCTCAGCATCATATCTCAAGGCAATTTGAAGGAGAGAAAGTACAGATGCCCTC 2640
QY 881 SerLeuProHisValLysLeuLys 888
Db 2641 ACCTGCTCATGTCAAACTGAAA 2664

RESULT 2
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. us20020042505A1el Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

Alignment Scores: 0 Length: 2772
Pred. No.: 4547.00 Matches: 888
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-810-796-5 (1-888) x US-09-825-147-1 (1-2772)
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QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrleuGlyGlyGlyGlyGly 40
Db 166 GACGGCTGCTACTGCTGGGCAACCGGGCGGCCACGCTGGGTGGCGGGGGGTGGCTG 225
QY 41 ArgGlySerArgArgGlyGlyGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 226 AGGAGAGCGCGCGGCGGCAAGAGGGGGCCGATGAGCCGTGGGGAACCGCTCTCT 285
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 286 TACACGATGACCAAGACCTCCGCGCAAGTCAAGTACCGCGGGTGACAACTACCTG 345
QY 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 346 TACAGGTGCTGAGAGAGACCCCGGGCTGGCGCTCATCTACACAGCTTCGTTTCTCTC 405
QY 101 LeuValPheGlyLysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 406 CTGTCTTGTGCTGCTGATTTGTCTAGTGTCTTCTACCTCCCTGAGCACCAAAATTG 465
QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 466 GCCTCAAGTTGGCTCTTGATCTCGAGTTGTGATGATGTGCTTGTGTTGGAGTTC 525
QY 141 IleIleArgIleTyrPheSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 526 ATCATTCGAATCTGCTGCTGGGGTGTGCTGTTCGATATGAGAGATGGCAAGAACTG 585
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValIleAlaSerIleAla 180
Db 586 AGGTGTGCTGAAAGCCCTTGTGTATGATACCAATTTCTTATCCGCTTCAATGACA 645
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuAspSerLeuArg 200
Db 646 GTTCTTTCGCAAAACTCAGGTAATATTTTGGCCAGCTCTGCACCTCAGAACTCTCGT 705
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyThrTrpLysLeuLeu 220
Db 706 TTCCTACAGATCTCCGCAATGGGCGCATGACCGCAAGGGAGGCACTTGGAAATTACTG 765
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrValTrpTyrIleGlyPheLeu 240
Db 766 GCTTCAGTGGTTTATGCTCAGCAAGAAATTAATACACACTTGTGATCAATGAGATTG 825
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 826 GTTCTATATTTTTCGCTTCCCTTGTCTATCTGCTGGAAGAAAGATGCCAATAAGCTTT 885
QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 886 TCTACATATGACAGATCCTCTGCTGGGGCACAAATTAATCACTATGCAACTATTTGGCTATGA 945
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 946 GACAAAGCTCCCTAACTTGGCTGGGCAAGATTCCTTTTCAGAGCTTTGGACTCTGGGC 1005
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1006 ATTTCTTCTTTCACCTTCCTCGGCAATTTCTGCTCAGGTTTTCATTTAAAGATACAA 1065
QY 321 GluGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340
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|----|------|--|------|
| Db | 1066 | GAACAACACCGCCAGAAACACTTTTGAGAAAAGAGAAACCCAGGCTGCCAACCTCATTTCAg | 1122 |
| Qy | 341 | CysVal1TrpArgSerTyrAlaAlaAspGluIlySerValSer1LeuAlaThrTrpIysPro | 360 |
| Db | 1126 | TGTGTGTGGCCGTAGTTAGCGACACTGATGGAATCGTTTCCATTGGCAACCTGGAGGCCA | 1185 |
| Qy | 361 | HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg | 380 |
| Db | 1186 | CACTTGAAGGCCCTTGACACACCTGGACGCTTACCATTACAAAGCTAAGTTTAAGAGCGCA | 1245 |
| Qy | 381 | ValArgMetAlaSerProArgGlyGlnSer1IleLysSerArgGlnAlaSerValGlyAsp | 400 |
| Db | 1246 | GTGGCCATGGCTAGCCGCCAGGGGCCAGAGTATTAAAGCCGCAACCCCTCAGTAGGTGAC | 1305 |
| Qy | 401 | ArgArgSerProSerThrAsp1LeuThrAlaGluGlySerProThrLysValGlnLysSer | 420 |
| Db | 1306 | AGGAGGTCCCCACAGCACCGACACTCACAGCCGAGGAGCATGCCACCAAGTCAGAAAGAGC | 1365 |
| Qy | 421 | TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro | 440 |
| Db | 1366 | TGGACCTTCAACAGCCGAACCCGCTTCCGGCCCTCGCTCCGCTCAAAAGTTCTCGAGCA | 1425 |
| Qy | 441 | LysProVal1IleAspAlaAspThrAlaLeuGlyThrAspAspVal1TyrAspGluLysGly | 460 |
| Db | 1426 | AAACCAAGTATGATGCTGACACAGCCCTTGGCAGCTGATGATTATGATGAAAAAGGA | 1485 |
| Qy | 461 | CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrVal1IleArgAla | 480 |
| Db | 1486 | TGCCAGTGGATGTATCATGTGAGAGACCTCACCCACCCTTAAACTGTCAATTCGAGCT | 1545 |
| Qy | 481 | IleArgGluMetLysPheHisValAlaLysArgGlyPheLysGluThrLeuArgProTyr | 500 |
| Db | 1546 | ATCCAAATTTATAAATTTGATGTTGCGAANAAGGAGTTTAAAGAAACATTACGTCATAT | 1605 |
| Qy | 501 | AspValLysAspVal1IleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle | 520 |
| Db | 1606 | GATGTAAAGATGTGATTAACAATATTCGTGCTGATCATGTGACATGTGTGACATTT | 1665 |
| Qy | 521 | LysSerLeuGlnThrArgValAspGln1IleLeuGlyLysGlyGln1IleThrSerAspLys | 540 |
| Db | 1666 | AAAACCTTCAACACAGCTGTGTGATCAAAATTTGTGAAAAGGGCAAAATCAATCAGATCAAG | 1725 |
| Qy | 541 | LysSerArgGluLys1LeuThrAlaGlnHisGluThrThrAspAspLeuSerMetLeuGly | 560 |
| Db | 1726 | AAGAGCGCAGAGAAATTAACAGCAGAAATGAGACCAACAGATCATCAGATATGCTCGGT | 1785 |
| Qy | 561 | ArgValValLysValGluLysGlnValGlnSer1IleGluSerLysLeuAspCysLeuLeu | 580 |
| Db | 1786 | CGGGTGGCTAAAGCTTGAANAACAGGTACAGTCCATGAAATCCAAAGCTGGACTGCTACTGA | 1845 |
| Qy | 581 | Asp1LeuTyrGlnIleValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe | 600 |
| Db | 1846 | GACATCTATCAACAGGTCTCTCGGAAAGGCTGTGCTCACACCTCGCTTGGCTTCATTC | 1905 |
| Qy | 601 | Gln1IleProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys | 620 |
| Db | 1906 | CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA | 1965 |
| Qy | 621 | AspLeuSerGlySer1LeuGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle | 640 |
| Db | 1966 | GATCTTTGGGTTCCCCACAAAACAAGTGGCTTATCCAGATCAACTAAGTGGCCAAATC | 2025 |
| Qy | 641 | SerArgGlyLeuGlnPhe1LeuThrProAsnGluPheSerAlaGlnThrPheTyrAla | 660 |
| Db | 2026 | TGCAGAGGCTGCAATTCATTCGAGCCCAATGAGTTCAGTGGCCAGACTTTCAGCGG | 2085 |
| Qy | 661 | LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer | 680 |
| Db | 2086 | CTTAGCCCTACTATGCACAGTCAAGCAACACAGTGCCAATTGATCAAGCATAGGCTCA | 2145 |
| Qy | 681 | AlaValAlaAlaThrAsnThr1LeuAlaAsnGln1LeuAsnThrAlaProLysProAlaAla | 700 |
| Db | 2146 | GCAGTGGCAGCCCAACACCATTTGCAACCAATTAATACGGCACCACCAAGCCAGCACCC | 2205 |

[illegible]

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RESULT 3
US-09-825-147-3
? Sequence 3, Application US/09825147
? Patent No. US20020042505A1
? GENERAL INFORMATION:
? APPLICANT: Hu, Yi
? APPLICANT: Kieke, James Alvin
? APPLICANT: Turner, C. Alexander Jr.
? APPLICANT: Nehls, Michael C.
? APPLICANT: Friedrich, Glenn
? APPLICANT: Zambrowicz, Brian
? APPLICANT: Sands, Arthur T.
? TITLE OF INVENTION: No. US20020042505A1el Human Ion Cha
? TITLE OF INVENTION: Polynucleotides Encoding the Same
? FILE REFERENCE: LEX-0160-USA
? CURRENT APPLICATION NUMBER: US/09/825, 147
? CURRENT FILING DATE: 2001-04-03
? PRIOR APPLICATION NUMBER: US 60/194,255
? PRIOR FILING DATE: 2000-04-03
? NUMBER OF SEQ ID NOS: 3
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 3
? LENGTH: 3111
? TYPE: DNA
? ORGANISM: homo sapiens
US-09-825-147-3

Alignment Scores:
Pred. No.: 0
Score: 4547.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%

length: 3111
Matches: 888
Conservative: 0
Mismatch: 0

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Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
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QY 21 AsnGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 225 GAGGGCTGTACTGCTGGGACCCGCGGCCACGCTGGTGGGCGGGGCGGGCTG 284
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 285 AGGAGACAGCCGCGGGGCAAGAGGGGGCCCGGATGAGCCCTGCTGGGAACCCGCTCTCT 344
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
DB 345 TACACGAGTAGCCAGAGCTGCGCGCCGCAACGCTCAAGTACCGCGGGGTGCAGAACTACCTG 404
QY 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheLeuIleTyrHisAlaPheValPheLeu 100
DB 405 TACAAAGTGTGGAGAGAACCCCGGCTGGGCTTCATCTAACCAAGCTTCCTGTTTCTC 464
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGlnHisThrLysLeu 120
DB 465 CTTCGCTTGGTTCCTGATTTGTCCAGTGTCTTCTACCATCCCTGAGCACACAAATTTG 524
QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB 525 GCCTCAAGTTGGCTCTTGATCTGAGATTGCTGATGATTGCTGCTTGGTGGAGCTT 584
QY 141 IleIleArgIleTyrPserAlaGlyCysCysArgTyrArgGlyTyrPglArgLeu 160
DB 585 ATCATTCGAATCTGGTCTGGGGTGTGCTGTGTGATATGAGGATGGCAAGAAAGCTG 644
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 645 AGGTTTGCTGAAAGCCCTTCGTGTATGATATACCATTTGTCTTATGCTTCATACCA 704
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 705 GTTGTTCGCAAAAACCTCAGGGTAATATTTTGCACGCTGCACACAGAGCTCCGT 764
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
DB 765 TTCCTACGAATCTCCGCAATGGTGGCATGGACCGAAAGGGAGGACCTTGGAAATTTACTG 824
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
DB 825 GGTTCAGTGGTTTATGCTCACACAGCAAGCAATTATCACAGCTTGATACATAGATTTTTC 884
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 885 GTTCTTAATTTTTCGCTTCCTTGTCTATCTGTGTGAAAAAGATGCCAAATTAAGAGATT 944
QY 261 SerThrTyrAlaAspAlaLeuThrTrpGlyTyrIleThrLeuThrTrpIleGlyTyrGly 280
DB 945 TCTACATATGCAATCTCTCTGCTGGGGCACAATTACATTGACACACTATTGGCTATGGA 1004
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 1005 GACAAAACTCCCTTACTGCTGGGGAAGATGCTTCTCAGAGCTTTCGACCTCTGGC 1064
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuValGln 320
DB 1065 ATTTCTTTTGTGGACTTCTGCGGCAATTCCTTGGCTCAGATTTTCATTAAGATACAA 1124
QY 321 GlnGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 1125 GAACAACACCGCCAGAAACCTTTGACAAAAGAAAGAACCCAGCTGCCAACCTCATTCAG 1184

QY 341 CysValTyrPargSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
DB 1185 TGTGTTGGCGTAGTACGAGCTGATGAGAAATTCGTTCATTTGCACTTGGACCTGGAAACCA 1244
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
DB 1245 CACTTGAAAGCCCTTGGACACACTGACCCCTACCAATCAGAAAGTAAAGTTTAAAGACGA 1304
QY 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
DB 1305 GTGCGATGGCTAGCCCGAGGGGCGAGATTAAGAGCCGCAAGGCTCAGTAGGTGAC 1364
QY 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
DB 1365 AGGAGTCCCCAAAGCACCCACATCACAGCCGAGGCGCATGCCCAAAGTCGACAAAGAC 1424
QY 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
DB 1425 TCGAGCTTCAAGCAGCAACCCGCTTCGCGCCCTCGCTGCGCTCAAAAGTTTTCAGCCA 1484
QY 441 LysProValIleAspAlaAspThrAlaLeuGlyTyrAspAspValTyrAspGluLysGly 460
DB 1485 AAACCAAGTATGATGATCTGACACAGCCCTTGGCAGCTGATGATGATGAAAAAGGA 1544
QY 461 CysGlnCysAspValSerValGlnAspLeuThrProProLeuLysThrValIleArgAla 480
DB 1545 TGCACATGATGATATACATGAGACCTCACCCACCATTTAAACTGTTCATTCGAGCT 1604
QY 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
DB 1605 ATCAGAAATTAATCAATTTTCATGTTCGAAACGGAAGTTTAAGAAACATTACGTCATAT 1664
QY 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
DB 1665 GATGTAAAGATGCTCAATGAAATATTTCTGTGCTATCTGGACATGTTGTGTGAATTT 1724
QY 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
DB 1725 AAAAGCTTCAAAACACCTGTGATCAAAATTTCTTGAAAGGCAATACATCAGATCAATAC 1784
QY 541 LysSerArgGluLysIleThrAlaGlnHisGluThrThrAspAspLeuSerMetLeuGly 560
DB 1785 AAGAGCGGAGCAAAATTAACAGCAGAAATGAGACACACACATCATCATGCTCGT 1844
QY 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
DB 1845 CGGTTGGTCAAGGTTGAAAAACAGTACAGTCCATGAAATCCAAAGCTGACCTGCTACTA 1904
QY 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
DB 1905 GACATCTATCAACAGCTCCTTCGGAAGGCTTCGCTCAACCCCTTCGCTTGGCTTCAATTC 1964
QY 601 GlnIleProProPheGluCysGlnGlnThrSerAspTyrGlnSerProValAspSerLys 620
DB 1965 CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAA 2024
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
DB 2025 GATCTTGGGTTTCGCAAAAACAGTGGCTGCTTATCCAGATCAACTATGTGCCAAATTC 2084
QY 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGlnPheSerAlaGlnIleThrPheTyrAla 660
DB 2085 TCGAGAGGCTCGAGTTCATTTGACGCCCAATGACATTCAGTCCCGACACTTTCACGCC 2144
QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
DB 2145 CTTCAGCCCTACTATGACAGTCAGCAAGCAACAGTGCATATGATGCAAAAGCATGGCTCA 2204
QY 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAspThrIleProLysProAlaAla 700
DB 2205 GCAGTGGCAGCCACCAACCATTTGCAAAACCAATTAATTAATGAGCAGCCAGCAAGCC 2264
QY 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGln 720

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QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeu 740
Db 2325 ACTCTGCACCTTAACCCCTGACAGGCTTACAGAAAGCATTTCTGACGTCACACCTGCTT 2384
QY 741 ValAlaSerLysGluAsnValGlnValAlaGlnIleSerAsnLeuThrLysAspArgSerMet 760
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QY 761 ArgLysSerPheAspMetGlyGlyGlnThrLeuLeuSerValCysPrometValProLys 780
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QY 781 AspleuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGlnGluLeuAsnIle 800
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QY 801 GlnLeuSerGlySerGluSerGlySerGlySerGlnAspPheArgProLysTrp 820
Db 2565 CAACTTCAGAGAGAGAGCAAGTGGCTCCAGAGGAGCAACAGATTTTACCCAAATGG 2624
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QY 841 ThrPheAspAlaIleAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
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QY 861 ThrGlnArgSerArgSerGlnSerIleCysLysAlaGlyGlnSerThrAspAlaLeu 880
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Db 2805 AGCTTGCCCTCATGTCAAACTGAAA 2828
RESULT 4
US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeda, Timothy James
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1e1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)-(2694)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-2
Alignment Scores:
Pred. No.: 0 Length: 2694
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 99.57% Indels: 9
DB: 10 Gaps: 1

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QY 81 TyrAsnValLeuGlnLuarArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
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 QY 361 H1SLLEuYsAlaLeuH1sThrCysserProThr----- 371
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 QY 372 AaG1LysLeuSerPheYsG1UaRgValAaRgMeLaSerProAaRgG1LysLeu 391
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 Db 1201 AAGAGCCGCAACACCTCAGTACAGAGGTGACAGAGGTCCCAAGCACCATCATCAGCCAG 1260
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 RESULT 5
 US-09-810-796-1
 ; Sequence 1, Application US/09810796
 ; Patent No. US20020102677A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jeda, Timothy James
 ; APPLICANT: ICGen, Inc.
 ; TITLE OF INVENTION: KCNO5, a No. US20020102677A1 potassium channel
 ; FILE REFERENCE: 018512-005010US
 ; CURRENT APPLICATION NUMBER: US/09/810, 796
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: US 60/190, 954
 ; PRIOR FILING DATE: 2000-03-21
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 3071
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human outwardly rectifying, voltage-gated
 ; NAME/KEY: CDS
 ; LOCATION: (10)..(2703)
 ; OTHER INFORMATION: KCNO5-1
 US-09-810-796-1
 Alignment Scores:
 Pred. No.: 0 Length: 3071
 Score: 4523.50 Matches: 886
 Percent Similarity: 98.89% Conservative: 1
 Best Local Similarity: 98.77% Mismatches: 1
 Query Match: 99.48% Indels: 9
 DB: 10 Gaps: 1
 US-09-810-796-5 (1-888) x US-09-810-796-1 (1-3071)


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QY      21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
      70 GAGCGCGCTGCTACTGCTGGGACCGCGCGGCGGACGCTTGATGGGCGGCGGCTGGCCCTG 129
QY      41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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QY      61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
      190 TACAGAGTACCGAGAGTCCGCGGCGCAACGTCAAGTACCGCGGCGGTGCAGAACTACCTG 249
QY      81 TyrAsnValLeuGluArgProArgGlyTyrTrpAlaPheLeuTyrHisAlaPheValPheLeu 100
      250 TACAACGCTGAGAGAGACCGCGGCTGGCGGTTCATCTACACGCTTCGTTTTCTTC 309
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Db 2170 GCCATCAAGCATCTGGCCCGAGCCAGAAACTCTGCACCTTAACCTTGACGCTTACAGCAA 2229

Qy 732 SerIeserAspValThrThrCysLeuValAlaSerIysGluAsnValGlnValAlaGln 751

Db 2230 AGCATTTCTGACGTACCCACCTGGCTTGTTCCTCCAAAGAAATATGTTTCAGTTGACAG 2289

Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGluThrIleu 771

Db 2290 TCAATCTCACCAAGACACCTTCTATGAGAAAGACTTTTACATGAGGAGGAAACTCTG 2349

Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791

Db 2350 TTGATCTCTCTGTCACATGGTGGCCGAAGGACTTTGGCAAAATCTTGTCTGTCAAAACCTG 2409

Qy 792 IleArgSerThrGluGluLeuAsnIleGlnIleuSerGlySerGlyIleuSerGlySerArg 811

Db 2410 ATCAGCTGCACCGACGAGAACTGATATACAACTTTCAAGGGAGTGAGTCAAGTGGCTCAGA 2469

Qy 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGlu 831

Db 2470 GGCAGCCAGATTTTACCCTCAATGGAGAGGATTCAAATGTTTATACTGATGAGAAAG 2529

Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851

Db 2530 GTGGGTCCCGAGACACGACACACACACTTTGATGCCGACCGCTGCCAGGAA 2589

Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871

Db 2590 GCTGCTTTCATCAGACTCTCTAAGCACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2649

Qy 872 LysAlaGlyIleuSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888

Db 2650 AAGCGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700

RESULT 6

US-09-813-148-1

: Sequence 1, Application US/09813148

: Patent No. US20020076809A1

: GENERAL INFORMATION:

: APPLICANT: STEINMEYER, Klaus

: APPLICANT: LERCHE, Christian

: APPLICANT: SCHERER, Constanze

: APPLICANT: SEEBOM, Guiscard

: APPLICANT: BUSCH, Andreas E.

: TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CENTRAL NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM

: FILE REFERENCE: 38005-119

: CURRENT APPLICATION NUMBER: US/09/813.148

: CURRENT FILING DATE: 2001-03-21

: PRIOR APPLICATION NUMBER: DE 100 13 732.6

: PRIOR FILING DATE: 2000-03-21

: PRIOR APPLICATION NUMBER: US 60/194,041

: PRIOR FILING DATE: 2000-04-03

: NUMBER OF SEQ ID NOS: 6

: SOFTWARE: PatentIn version 3.0

: SEQ ID NO 1

: LENGTH: 3074

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-813-148-1

Alignment Scores:

Pred. No.: 0

Score: 4513.50

Percent Similarity: 98.778

Best Local Similarity: 98.668

Query Match: 99.268

DB: 10

Length: 3074

Matches: 885

Conservative: 1

Mismatches: 2

Indels: 9

Gaps: 1

US-09-810-796-5 (1-888) x US-09-813-148-1 (1-3074)

1 MetLysAspValGluSerGlyArgValIleuLeuAsnSerAlaAlaIlaArgGly 20

| | | | |
|----|------|---|------|
| Db | 215 | ATGAGGATGTCAGTCCGGCCGGGCGACGGTCTCTCAACTCGGACGCCCGCAGGGC | 274 |
| QY | 21 | AspGlyLeuLeuLeuLeuLysThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu | 40 |
| Db | 275 | GACGGCTCTACTCTGGGACCCCGCGCGCCACCTTGGTGGCGCGCGGTGGCTTG | 334 |
| QY | 41 | ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer | 60 |
| Db | 335 | AGGGAGACCCCGCGGCGCAACGAGGGCGCGGATGAGCTGTGGGAAGCCCTCTCT | 394 |
| QY | 61 | TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu | 80 |
| Db | 395 | TACACGATAGCCAGAGGTGCGCGGCAACGTCAGTACCGCGGGTGGAGAACTACTTG | 454 |
| QY | 81 | TyrAsnValLeuGluArgProArgGlyTyrPheLeuPheLeuTyrHisAlaPheValPheLeu | 100 |
| Db | 455 | TACAACTGCTGGAGAGACCCCGCGGTGGGCTTCATCTACACGCTTTCGTTTCTCTC | 514 |
| QY | 101 | LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu | 120 |
| Db | 515 | CTTCTCTTGGTGGCTGATATTGGTCAGAGTGTTCATCCATCCCGACGACCAAAATTG | 574 |
| QY | 121 | AlaSerSerCysLeuLeuLeuLeuLysPheValMetIleValValPheGlyLeuGluPhe | 140 |
| Db | 575 | GCCCAAGTCCCTCTGATCTCTGAGTTCTGATGATGTCTCTTGGTTGGAGTTC | 634 |
| QY | 141 | IleIleArgIleTyrPheSerAlaGlyCysCysArgTyrArgGlyTyrPheGlnArgLeu | 160 |
| Db | 635 | ATCATTCGAATCTGGTCTGGCGGTTGTCTGTCTGCATATAGAGATGCCAGAGAGACTG | 694 |
| QY | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla | 180 |
| Db | 695 | AGGTTGCTCGAAAGCCCTTCTGGTATTAATACCATTTGTTATCGCTTCAATAGCA | 754 |
| QY | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 |
| Db | 755 | GTTGTTTCTCGAAAACTCAGGGTAATATTTTGGCACGTCGCACTCAGAGTCTCCT | 814 |
| QY | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu | 220 |
| Db | 815 | TTCCTACAGATCTCCCAATGGTGCGATGGACCGAAGGGAGGCACCTTGCAAATTACTG | 874 |
| QY | 221 | GlySerValValTyrAlaHisSerLysGluLeuLeuIleThrAlaTyrPheIleGlyPheLeu | 240 |
| Db | 875 | GGTTCACTGGTTATGCTCAGACAGAAAGAAATATTCACAGCTTGGTACATAGCAATTTTG | 934 |
| QY | 241 | ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 |
| Db | 935 | GTTCTTATTTTTCGTCTTCCCTTGTCTATCTGGTGGAAGGATGCCAAATAAGAGTTT | 994 |
| QY | 261 | SerThrTyrAlaAspAlaLeuTyrTrpGlyTyrThrIleThrLeuThrThrIleGlyTyrGly | 280 |
| Db | 995 | TCTACAAATGACAGATGCTCTCTGGTGGGACATTTACATTGACAACTATTGGCTATGGA | 1054 |
| QY | 281 | AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly | 300 |
| Db | 1055 | GACAAAGCTCCCTACTCTGGCTGGGAAGATTCCTTCTGCAGCCTTGGCACTCTTGGC | 1114 |
| QY | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 |
| Db | 1115 | ATTTCCTTCTTCCACTTCTCCCGCGCATTCCTTGGCTCAGAGTTTGGATTTAAAGTACAA | 1174 |
| QY | 321 | GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln | 340 |
| Db | 1175 | GAACAACACCGCGAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCCAACCCTATTCCAG | 1234 |
| QY | 341 | CysValIleTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro | 360 |
| Db | 1235 | TCTGTTGGCGTAGTACCAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAACCA | 1294 |
| QY | 361 | HisLeuLysAlaLeuHisThrCysSerProThr----- | 371 |

| | | | |
|----|------|---|------|
| Db | 160 | CCACCCCGGGAGCGGGCGCTGATCGCCGGCTCCGAGGCCCCCAAG-----CGC | 210 |
| OY | 37 | GLYGLYGLYLeuArgGluSerArgArgLYLSGLINGLYAlaArgMetSerLeuLeuGLY | 56 |
| Db | 211 | GCCACCATCTCAGCAACCTCGCGGGCGGCGCGCGCGCC-----GGG | 255 |
| OY | 57 | LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgGVal | 76 |
| Db | 256 | AAAGCC-----CCCAAGCGCAAGCCCTTTCACGCCAAGCTG | 291 |
| OY | 77 | GlnAsnTyrLeuTyrAsnValLeuGlnuArgProArgLYTTPAlaPheLeuThrHisAla | 96 |
| Db | 292 | CAGAAATTCTCTACAGCAAGTGTGGAGCGCGCGCGGTGGCGCTTCACTTACACAGCC | 351 |
| OY | 97 | PheValPheLeuLeuValPheGLYsLeuIleLeuSerValPheSerThrIleProGlu | 116 |
| Db | 352 | TACGTGTTCTCTCGGTGTTTTCTCTCGCTCGTGTGTGTGTGTTTCCACCTACAGAGG | 411 |
| OY | 117 | HisThrLysLeuAlaSerSerCysLeuLeuIleLeuGlnPheValMetLeuValPhe | 136 |
| Db | 412 | TATAGAAAGAGCTCGAGCGGGCCCTTACATCTCGGAATGTGACTATCTGTGGTTT | 471 |
| OY | 137 | GLYLeuGlnPheIleLeuArgLLeuTrpSerAlaGlyCysCysArgTyrArgLYTrp | 156 |
| Db | 472 | GGCGTGGAGTACTTCGTCCGATCTGGCGCCGACAGCTGCTGTCGGTACCGTGGCTGG | 531 |
| OY | 157 | GlnLYArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle | 176 |
| Db | 532 | AGGGGGGGCGTCAAGTTGGCCCGGAACCGTTCTGTGTGATTGATCATCGTGTCTAC | 591 |
| OY | 177 | AlaSerIleAlaValValSerAlaLysThrGlnLYsnIlePheAlaThrSerAlaLeu | 196 |
| Db | 592 | GCCCTCAATTGCGGTGCGCGCCCGCTCCAGGCAACGCTTGGCACATCTGCGTC | 651 |
| OY | 197 | ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgLYLYThr | 216 |
| Db | 652 | CGAGCGCTCGCTTCTCGCAGATTCTGGGTGTGATTCGCAAGAGCGCGGGAGGCAAC | 711 |
| OY | 217 | TrpLysLeuLeuGLYSerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpYr | 236 |
| Db | 712 | TGGAACTGCTGGGCTCTGTGCTTATGCCACAGCAAGAGCGTGGTACCTGCTGATC | 771 |
| OY | 237 | IleGLYpHeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla | 256 |
| Db | 772 | ATCGGCTCTTTGTCTCATCTCGCTCGTTCTGGTGTACTTGGCAAGAACGGGGAG | 831 |
| OY | 257 | AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTrpLYThrIleThrLeuThrThr | 276 |
| Db | 832 | AACGACACATTGACACCTACCGGGATGCACTGTGGTGGGCTGATCAGCTGATCCAC | 891 |
| OY | 277 | IleGLYTYrGLYAspLysThrProLeuThrTriPLeuGlnArgLeuLeuSerAlaGlyPhe | 296 |
| Db | 892 | ATTGGTACGGGACACAGTACCCCAAGCTGGAGCGGCGGCTCTTTCGGCAACCTTC | 951 |
| OY | 297 | AlaLeuLeuGLYIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla | 316 |
| Db | 952 | ACCCATCATGGTGTCTCTTCTTCCGCGTGGCGAGGATCTTTGGGGTGTGGGTTTGGC | 1011 |
| OY | 317 | LeuLysValGlnGlnGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla | 336 |
| Db | 1012 | CTGAAGGTTTCAGAGACGACACAGCGCAAGCACTTGGAGAAGAGCGGAAACCGGAGCA | 1071 |
| OY | 337 | AsnLeuIleGlnCysValTyrPArgSerTyrAlaAlaAsp----- | 349 |
| Db | 1072 | GCCCTGATCTACGTGGCGTGGAGATTTCAGCCACCAACCTCTCGCGGCAAGACTGGAC | 1131 |
| OY | 350 | -----GluLysSerValSerIleAlaThrTriPlys----- | 359 |
| Db | 1132 | TTCACGTGGCACTACTACAGAGCAACGCGTACCGCATGTACAGTTGCGAACTGAA | 1191 |
| OY | 360 | -----ProHisLysValAlaLeuHisThr----- | 367 |
| Db | 1192 | ACCTACGGGGGCTCCAGACCTTATGCCCGCGCTGAACCAAGTGTGAGCTGTGAGAAACCTC | 1251 |

| | | | |
|----|------|---|------|
| OY | 367 | ----- | 367 |
| Db | 1232 | AAGAGTAAATCTGAGACTCGCTTTCAGAGAGACCCCGCGCGGAGCGCTCCAGTAA | 131 |
| OY | 368 | ----- | 368 |
| Db | 1312 | GGCAGCCCGTCGACAGAGGCCCTGTGTGTGATCTCGCCCGACGCTCTAGCCGAGAGTTC | 137 |
| OY | 376 | SerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln | 395 |
| Db | 1372 | AGTTTGAAGAAGATCTGCTC---TTCCTCACCCCCGAGCGGTGGCTCCCAAGGGAGAGGG | 142 |
| OY | 396 | AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGlnGlySer | 413 |
| Db | 1429 | TCCCGCGAGCCCGACAGACTGTGAGGGGGTCCACCACCGCCGACACAGCTCCGAGCGACAC | 148 |
| OY | 414 | ProThrLysValGlnLysSerThrSerPheAsnAspArgThrArgPheArgProSerLeu | 433 |
| Db | 1489 | CCCGAGCAAGTGGCCCAACAGAGCTGGAGCTTCGGGGACCCGACCGGGGACGCCAGCGCTTTC | 1541 |
| OY | 434 | ArgLeuLysSerSerGlnProLysProValIleAspAlaSerThrAlaLeuGlyThrAsp | 453 |
| Db | 1549 | CGCATTCAGAGGGTGGCGGCTCACCGCAG---AACTCAGAAAGCAAGCGTCCCGGAGAG | 1601 |
| OY | 454 | AspValTyrAspGlnLysGlyLysGlnLysAspValSerValGlnAspLeuThrProPro | 473 |
| Db | 1603 | GACATTGTGGATGACACAGAGCTGCCCTCCGAGATTGTGCACCGAGAGCTGACCCCGGC | 1661 |
| OY | 474 | LeuLysThrValIleArgAlaIleArgIleMetLysPheIleValAlaLysArgLysPhe | 493 |
| Db | 1663 | CTCAAAAGTCAGACATCAGACGCGGTGTGTCTCATGCGGTCTGTGTCACACCGGAAGTTC | 1722 |
| OY | 494 | LysGlnThrLeuArgProTyrArgAspValLysAspValIleGlnGlnTyrSerAlaGlyHis | 513 |
| Db | 1723 | AAGAGAGCGCTCGCGGCTTACGAGCTGTGAGACCTCATCGACGAGTCACTCAACCCCGCAC | 1783 |
| OY | 514 | LeuAspMetLeuCySarGlyIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLys | 533 |
| Db | 1783 | CTGACATGCTGTGCCGAATTAAAGCCTGCATGCCAGAGTGGACCAAGTCTGTGGCGGG | 1842 |
| OY | 534 | GlyGlnIleThrSerAspLysLysSerArgGlnLysIleThrAlaGlnHisGlnThrThr | 553 |
| Db | 1843 | GGCCGACGATCAGCGAC---AAGGACCGACCAAGGGCCCGCGGAGGGCGGACTGCCC | 1899 |
| OY | 554 | AspAspLeuSerMetLeuGlyArgValValLysValGlnLysGlnValGlnSerIleGln | 573 |
| Db | 1900 | GAGAGACCCCGCATGTATGGAGCGGCTCGGAGGTGAGAAACAGGCTTGTTCATGTGAG | 1959 |
| OY | 574 | SerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaSer | 593 |
| Db | 1960 | AAGACACTGGACTTCTCTGGTGAATATCTTACATGACG---CGGATGGGC----- | 2004 |
| OY | 594 | AlaLeuAlaLeuAlaSerPheGlnIleProProPheGlnLys----- | 607 |
| Db | 2005 | -----ATCCCCCGCAGAGACCGACGAGCGCTACTTTGGGGCC | 2040 |
| OY | 608 | -----GlnGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGly | 624 |
| Db | 2041 | AAAGACCCCGGAGCGCGCGCCCGCTTATCACACACCGCGAGACGCGCGGAG----- | 2091 |
| OY | 625 | SerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeu | 644 |
| Db | 2092 | CATGTTCGACAGCGACGGGTGCATTGTTCACAGATCGTCCGCTCCACGACGCTCCACGGGC | 2148 |
| OY | 645 | GlnPheIleLeuThrProAsnGlnPheSerAlaGlnThrPheTyrAlaLeuSerProThr | 664 |
| Db | 2148 | ----- | 2148 |
| OY | 665 | MetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaIle | 684 |
| Db | 2148 | ----- | 2148 |


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QY 383 MetalaserProArgIyGlnSerIleLysSerArgGlnAlaserValGlyasp----- 400
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Db 1246 TTTCACAGCCCCCAGGCGATGCGCCAAAGGAAGGGGTCTCCCCAGCCAGACGCTC 1305
QY 401 ArgArgSerProSerThrAspIleThrAlaGluLysSerProThrLysValGlnLysSer 420
    ::::::::::::::::::::
Db 1306 CCGGGGGCCCCCAGTCGAGTACAGTCTTATGATGACAGCCCGACAGAGTGGCCCAAGAC 1365
QY 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerGlnPro 440
    ::::::::::::::::::::
Db 1366 TGGAGCTTTGTGTGACCCAGCCGACAGCCAGGCTTTCCGATCAAGGTCCTCATCC 1425
QY 441 LysFroValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGlnLysGly 460
    ::::::::::::::::::::
Db 1426 CCGCAGATTTCAGAACGAGCTCCCT---GGGAGAGCAATCGTTGAGAGCAGACAGAC 1482
QY 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
    ::::::::::::::::::::
Db 1483 GTTAACTGCGAGTTTGTACTGAAGATCTTACCCCTGCGCTCAAGATTAGCATCAGAGCT 1542
QY 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGlnThrLeuArgProThr 500
    ::::::::::::::::::::
Db 1543 GTCTGTGTATCCGCTCTTGATCTAAGCGCAAGTTCAAGAGAGTCTGGCCCATAT 1602
QY 501 AspValLysAspValIleGluGlnTyrSerAlaGlnHisLeuAspMetLeuLysArgIle 520
    ::::::::::::::::::::
Db 1603 GATGTGATGAGCATCGAATCGAAGTACTCGCTGCGACACTTGGAATGTGTGCCGCAATC 1662
QY 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlnLysGlnIleThrSerAspLys 540
    ::::::::::::::::::::
Db 1663 AAGAGCTGTGAGTCCAGAGTGCAGACCAATGTGGGGGGGGCCCAACAATAACGAT--- 1719
QY 541 LysSerArgGlnLysIleThrAlaGlnHisGlnThrThrAspAspLeuSerMetLeuGly 560
    ::::::::::::::::::::
Db 1720 AAGAGTCCGACCAAGAGCCGACGGAAGAGAGCTGCCCGCAAGACCCAGCATGATGGGA 1779
QY 561 ArgValValLysValGlnLysGlnValGlnSerIleGlnSerLysLeuAspCysLeuLeu 580
    ::::::::::::::::::::
Db 1780 CCGCTGTGGGAGGTGGAGAAACAGGTCTTGCTCAATGGAAGAAAGATCGACTTCTGGTG 1839
QY 581 AspIleTyrGlnGlnValIleuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerHe 600
    ::::::::::::::::::::
Db 1840 AGCATCTATACACAG---AGATATGGC----- 1863
QY 601 GlnIleProProPheGlnCys-----GluGlnThrSer 611
    ::::::::::::::::::::
Db 1864 ---ATCCCAACAGACAGACAGAGCCTATTTTGGGGCCAAAGAGCCTGACCCGCCACCA 1920
QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
    ::::::::::::::::::::
Db 1921 CCTTACCACAGCCCAAGAGACAGCCCGTGAC-----CATGCAGACAAACCATGCGTGT 1971
QY 632 ---LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeu 648
    ::::::::::::::::::::
Db 1972 ATCATTAAGATCTCTCCGCTCCACACGCTCT----- 2001
QY 649 ThrProAsnGlnPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGln 668
    ::::::::::::::::::::
Db 2002 ---ACGGCCAGAGAGAACTACGACACACCCCGAGCATC-----CCC 2040
QY 669 AlaThrGlnValProIleSerGlnSer 677
    ::::::::::::::::::::
Db 2041 CCTGCCCACTGTCTCTCCACCTCG 2067

RESULT 9
US-10-128-870-26
: Sequence 26, Application US/10128870
: Patent No. US20020168724A1
: GENERAL INFORMATION:
: APPLICANT: Bliane, Michael A.
: APPLICANT: Dworetzky, Steven
: APPLICANT: Grikoff, Valentin K.
: APPLICANT: Levesque, Paul C.
```

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: APPLICANT: Little, Wayne A.
: APPLICANT: Neubauer, Michael G.
: APPLICANT: Yang, Wen-Pin
: TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
: FILE REFERENCE: DC58ADIV
: CURRENT APPLICATION NUMBER: US/10/128,870
: PRIORITY FILING DATE: 2002-04-24
: PRIOR APPLICATION NUMBER: 09/105,058
: PRIOR FILING DATE: June 26, 1998
: PRIOR APPLICATION NUMBER: 60/055,599
: PRIOR FILING DATE: August 12, 1997
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: Patentl Ver. 2.1
: SEQ ID NO 26
: LENGTH: 2565
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-128-870-26

Alignment Scores:
pred. No.: 1,5e-147 Length: 2565
Score: 1587.50 Matches: 386
Percent Similarity: 54.61% Conservative: 106
Best Local Similarity: 42.84% Mismatches: 244
Query Match: 34.91% Indels: 165
Gaps: 28

US-09-810-796-5 (1-888) x US-10-128-870-26 (1-2565)
QY 3 AspValGlnSerGlyArgValLeuLeuAsnSerAlaAlaArgGlyAspGly 22
    ::::::::::::::::::::
Db 91 GACCTGGAGCA-----GTCACCTTGGCGTGGGGCCGAGCCGCAAGAGCGG 141
QY 23 LeuLeuLeuGlnThrArgAlaIleThrLeuGlnGlyGlyGlyGlyLeuArgGlu 42
    ::::::::::::::::::::
Db 142 ACCCTCTGCTG-----GAGGGCGGCGCGCCGACGAGCGG 177
QY 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
    ::::::::::::::::::::
Db 178 CACGGAGAGACCCCGCAGAGGC-----ATCGGCTCTGGCCCAAGACCCGCTGAGCGC 231
QY 62 ThrSerSerClnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
    ::::::::::::::::::::
Db 232 CCAAGTCAAG-----AGAAACAAGCCCAAGTACCGGGGCAATCCAACTTGATCTAC 282
QY 82 AsnValLeuGlnArgProArgGlyTyrPalaPheIleTyrHisAlaPheValPheLeuLeu 101
    ::::::::::::::::::::
Db 283 GACGCCCTGGAGACCGCGGGGCTGGCGCTGCTTACCAACGCGTGTGTTCTGATT 342
QY 102 ValPheGlnCysLeuIleLeuSerValPheSerThrIleProGlnHisThrLysLeuAla 121
    ::::::::::::::::::::
Db 343 GTTCCTGGGGTCTTGATTTGCTGTCTGCTGCTGACCAATTCAGAGAGTGGAGACTGTCTG 402
QY 122 SerSerCysLeuLeuIleLeuGlnPheValMetIleValValPheGlyLeuGlnPheIle 141
    ::::::::::::::::::::
Db 403 GGAGACTGGCTCTCTTACTGGAGACATTTGCTATTTTCACTTTTGAGCGCACTTGCT 462
QY 142 IleArgIleThrSerAlaGlnCysCysArgTyrArgGlyTyrPalaArgGlnArg 161
    ::::::::::::::::::::
Db 463 TTGAGGATCTGGGCTGCTGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
QY 162 PheAlaArgLysProPheGlnValIleAspThrIleValLeuIleAlaSerIleAlaVal 181
    ::::::::::::::::::::
Db 523 TTTCGACAGAACCCCTCTGTCATGTGGACATCTTTGTGCTGATGCTGTGCCAGTG 582
QY 182 ValSerAlaLysThrGlnLysAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
    ::::::::::::::::::::
Db 583 GTTGTCTGGAAACCAAGCAATGTTCTGGCCACCTCC---CTGGCAACCTGGCGCTTC 639
QY 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeuGly 221
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Db 640 CTGCAATCTCGCATGCTCGGATGAGACCGAGAGGTGGGCACTGGAAGCTTCTGGGC 699
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QY 222 SerValValYrAlaHisSerLysGluLeuLeuIleThrAlaTrpTyrIleGlyPheLeuVal 241
DB 700 TCACCCATCTGTCGCCACAGCAAGAACTCATACGCGCTGTATAGTGTTCCTGACA 759
QY 242 LeuIlePheSerPheLeuValTyrLeuValGluLysAspAla----- 256
DB 760 CTCATCTCTTCTTCTTCTTCTGCTACTGCTGTGAGAAAGACGTCCAGAGGTGCATGCA 819
QY 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpIleGlyThr 271
DB 820 CAAGAGAGAGATGAAGAGAGATTTGAGACCTATGCAGATGCCCTGTGGGGGCTCTG 879
QY 272 IleThrLeuThrTrpIleGlyTyrGlyAspLysThrProLeuThrTyrLeuGlyArgLeu 291
DB 880 ATCACACTGCCCATTTGGCTATGGAGACACAGACACCAAAACGGGAGAGCGCTCTG 939
QY 292 LeuSerAlaGlyPheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeu 311
DB 940 ATTCGCCGACCTTTCTCTTATTTGGCGTCTCTTTTGGCTTCCGCTCCAGCGGCACTCTG 999
QY 312 GlySerGlyPheAlaLeuLysValIleGluGlnHisArgGlnLysHisPheGlyLysArg 331
DB 1000 GGGTCCGGGCTGCGCTCAAGGTGCAGGAGCAACCGTCAGAGACACTTTGAGAAAGG 1059
QY 332 ArgAsnProAlaAlaAsnLeuIleGlnCysValTyrPargSerTyrAlaAlaAspGluLys 351
DB 1060 AGGAAGCCAGCTGCTGAGCTCATTTTCAAGCGTCCGTGAGGTATTATGCTCAACCAACCC 1119
QY 352 SerValSer-----IleAlaThrTrpLys-----ProHisLeu 362
DB 1120 AGGATTTGACGCTGTGGGACACATGAGATTTTATGATCAGTGTCTCTTCTCTTCTCTC 1179
QY 363 LysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArgValArg 382
DB 1180 AGGAAGAACAAGCTGGAGGACGATCCAGCCAAAGCTGGCTCTTGGATCGGTTCCG 1239
QY 383 MetIleSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArg 402
DB 1240 CTTCCTATCTCTGTTGATGCACTATA-----GGAAGCTATT 1281
QY 403 SerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTrpSer 422
DB 1282 ACCCTCTCATGTGTAGATGCCATAGACAAAGTCTCTTAAGAACCAAGCCTGTGGC 1341
QY 423 PheAsnAspArgThrArgPheArgProSerLeuArgLeuLys----- 436
DB 1342 TTAAACATTAAGAGCGTTTCGACGCGCTCCGATGAAGCCCTACGCTTCTGCGAC 1401
QY 437 SerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyr 456
DB 1402 AGTTCTGAA-----GATCGCGGACAGGT-----GACCCCATGGCG 1437
QY 457 AspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThr 476
DB 1438 GAAGACAGGCGCTATGGCATGCTCCCATCAGACATGATCCCATCCAGAGGCC 1497
QY 477 ValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThr 496
DB 1498 GCCATCCAGCGCTGAGATTTCTACATTCCTCTATTAATAAAATTCAGAGGACT 1557
QY 497 LeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMet 516
DB 1558 TTGAGGCTTACGATGTGAAGATGTGATGAGCATATTCTCCGGGCACTCTCGACATG 1617
QY 517 LeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIle 536
DB 1618 CTTTCAGAGATTAAGACTTTCAGAGAGATATGATTTTCAACCCCTGACCTCC 1677
QY 537 ThrSerAspLysLysSerArg----- 543
DB 1678 TCCACGCCAAACACAGAAAGTCTCGAAAGGCTGACATTCACCTTCCATCCACGAA 1737
QY 544 -----GluLysIleThrAlaGlnHisGluThr-----AspAspLeuSer 557

DB 1738 TCATCCAGAGATGACATATGATGACACCAATCCATCAGAAATCGAAGACCAAGC 1797
QY 558 MetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAsp 577
DB 1798 ATGATGGGGAAGTTTCTTAAGTTGAAAGACAGGTTGAGACATGGGAGAGAGCTGGAC 1857
QY 578 CysLeuLeuAspIleTyrGlnGlnValLeuArg----- 588
DB 1858 TTCCTGTGATATGACATGACACATGAGAACGCTTGACAGGTGCAGGTCAAGGATAT 1917
QY 589 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPhe 605
DB 1918 TACCCACCAAGGCGACCTCTCTG-----CCACCT 1947
QY 606 GluCysGluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySer 625
DB 1948 GAAGCAGAGAGAGAGAGAGACACACAGGATATTC-----GATTTGAAACCATCATCTGCAC 2004
QY 626 AlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGln 645
DB 2005 TATTCTAGACAGGCGCCCGGACACACCTTACAGCTTCCAC----- 2046
QY 646 PheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMet 665
DB 2047 ---CAGTGACCAATGACAAAGTCAACCCCTATGGGTTTTCGACATGACCT----- 2097
QY 666 HisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAlaThr 685
DB 2098 -----GTAACCTCCCGCCGAGGGGACCAGTCTGGAAGGTTCAAGGCACT 2145
QY 686 AsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGln 705
DB 2146 -----CCTCTTCTTCTGACCAACAGATGTGGAG 2175
QY 706 IleProProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisProAsn 725
DB 2176 AGGCCACAGGCTCGCTATCTGACTCTCTCGACTCCGACGAGTGCACGCTCCAC---TCC 2232
QY 726 ProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerLysGlu 745
DB 2233 CAGGCTGACCTGCGAGGGCCCTACTCTGAC----- 2262
QY 746 AsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAsp 765
DB 2263 CGAATTCGCCCGGCGAC-----AGACGTGACATCAGC 2295
QY 766 MetGlyGlyLeuThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSer 785
DB 2296 CGAAGAGGTGACACACCTCTGCTCTG----- 2322
QY 786 LeuSerValGlnAsnLeuIleArgSerThrGluGlnLeuAsnIleGlnLeuSerGlySer 805
DB 2323 ATGTGCGTCAACAC-----GAGGAGCTGGAGAGGTCTCCAAAGTGGCTTC 2367
QY 806 GluSerSerGlySerArgLysSerGlnAspPheTyrPro-----LysTrpArg 821
DB 2368 AGCATCTCCAGACAGAGAGATATGTTGCGCCCAATGGGGGTCGAGCGAGATG 2427
QY 822 GluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAspThr 841
DB 2428 AGGAGAGAGCGGTCTGCGCGAC-----GCTGAGACGACACAGACAGGAGCC 2478
QY 842 Phe 842
DB 2479 TTC 2481

RESULT 10
US-10-128-870-5
; Sequence 5, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Bلمانar, Michael A.

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; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58adiV
; CURRENT APPLICATION NUMBER: US/10/128,870
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 900
; TYPE: DNA
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-10-128-870-5

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Alignment Scores:
Pred. No.: 1,41e-110 Length: 900
Score: 1207.50 Matches: 227
Percent Similarity: 83.88% Conservative: 28
Best Local Similarity: 74.67% Mismatches: 40
Query Match: 26.56% Indels: 9
DB: Gaps: 2

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US-09-810-796-5 (1-888) x US-10-128-870-5 (1-900)

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QY 56 GlyLysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArg 75
DB 13 GGGAAAGCCC-----CCGAAGCGCAAGCCCTTCTACCCCAAG 48
QY 76 ValGlnAsnTyrLeuTyrAsnValLeuGlnArgProArgGlyTyrPalapheleTyrHis 95
DB 49 CTGCAAGATTCTCTACACAGCTGTAGAGCGGCCCGCGCGGCGGCTTCATCTACCAAC 108
QY 96 AlaPheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerThrIlePro 115
DB 109 GCCTACGTTCTCTTAGTCTTCTCCTGCTTGTGCTTCTGTTTCCACCAATCAAG 168
QY 116 GluHisThrLysLeuAlaSerSerCysLeuLeuLeuGluPheValMetIleValVal 135
DB 169 GAGTACGAGAAAGAGCTCTGAGGCGGCCCTTACATCTTGGAATGCTGACTATCGTGT 228
QY 136 PheGlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGly 155
DB 229 TTGGGCTGTAGTACTTGTGGAGATCTGGGCTGAGGCTCTGCTGCGGATCGAGGC 288
QY 156 TrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeu 175
DB 289 TGGAGGGCGAGCGCTCAAGTTTCCAGGAAGCGCTTCTGTGATGATGATCATGTGCTG 348
QY 176 IleAlaSerIleAlaValIleSerAlaIleThrGlnLysAsnIlePheAlaThrSerAla 195
DB 349 ATTGCTCCTACTTCTGCTGCGGCTGCTGCCAGGGCAATGCTTGGCCACATCTCGC 408
QY 196 LeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGly 215
DB 409 CTTCGAGCGTGGGCTTCTTGCACAAATCTTGGGATGATCCGTAAGGAGCGGAGGCTGCG 468
QY 216 ThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrp 235
DB 469 ACCTGGAAGCTCTTGGAGTCGTAGTCTACGCTACAGCAAGAGCGTGTGACTGCGTGG 528
QY 236 TyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAsp 255
DB 529 TACATTGGCTTCTCTGCTCATCCTGCGCTCATTTCTGTGTTACTTGGAGCAAAAGGT 588

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QY 256 AlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThr 275
DB 589 GAGATGACCACTTTTACACCTTACGACATGACATCTGGGGGCTGTGATCACCCTGACG 648
QY 276 ThrIleGlyTyrGlyLysAspLysThrProLeuThrTrpLeuGlyArgLeuSerAlaGly 295
DB 649 ACCATTGGCTACGGGGGCAAGTACCTCCAGACCTGGAGCGGAGGCTGTGCGACGACC 708
QY 296 PheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPhe 315
DB 709 TTTACCTCATTTGGTGTCTGCTTCTTCTGCTTCTGCTGCGCATTTTGGGATCCGGCTT 768
QY 316 AlaLeuLysValGlnGlnLysArgGlnLysHisPheGluLysArgArgAsnProAla 335
DB 769 GCCGTGAAGTCCAGAGAGCAGCATCGCAAAACACTTTGAGAAAGCGGAGAACCTGCG 828
QY 336 AlaAsnLeuIleGlnCysValTyrPargSerTyrAlaAlaAspLysSerValSerIle 355
DB 829 GCAGGTGTGATCAGTCTGCTGCGAGATTTCTATGCTACTAACCCTCAGCAGCAGCTG 888
QY 356 --AlaThrTrp 358
DB 889 CACTCCACTGTG 900

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RESULT 11
US-10-128-870-3
; Sequence 3, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blauar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58adiV
; CURRENT APPLICATION NUMBER: US/10/128,870
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-10-128-870-3

```

```

Alignment Scores:
Pred. No.: 5.57e-110 Length: 900
Score: 1201.50 Matches: 226
Percent Similarity: 83.55% Conservative: 28
Best Local Similarity: 74.34% Mismatches: 41
Query Match: 26.42% Indels: 9
DB: Gaps: 2

```

US-09-810-796-5 (1-888) x US-10-128-870-3 (1-900)

```

QY 56 GlyLysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArg 75
DB 13 GGGAAAGCCC-----CCGAAGCGCAAGCGCTTCTACCCCAAG 48
QY 76 ValGlnAsnTyrLeuTyrAsnValLeuGlnArgProArgGlyTyrPalapheleTyrHis 95
DB 49 CTGCAAGATTCTCTTACACAGCTGTGAGCGGCCCGCGGCGGCTTCACTCATCTACAC 108

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